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OM protein - protein search, using sw model

Run on: September 24, 2004, 14:02:27 ; Search time 51.308 Seconds
(without alignments)

Title: US-10-661-784-3

Perfect score: 687

Sequence: 1 GSGKDFVQPPTKICVGCPRD.....VPWERKIKYPTVTVNHWEECF 127

Scoring table: BLOSUM62

Gapext: 0.5

Searched: 1586107 seqs, 28547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database : A_GenSeq_29Jan04:*

1: genseqp_980s:*

2: genseqp_19s:*

3: genseqp_200s:*

4: genseqp_2001s:*

5: genseqp_2002s:*

6: genseqp_2003as:*

7: genseqp_2003bs:*

8: genseqp_2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

1	618	90.0	123	3	AAY95426	Human hig
2	618	90.0	304	6	ABP70801	Human ext
3	618	90.0	322	6	ABP70799	Human ext
4	618	90.0	329	6	ABU9044	Human pro
5	618	90.0	358	6	ABP70800	Human ext
6	618	90.0	390	6	ABU99149	Novel hum
7	618	90.0	398	6	ABU99143	Novel hum
8	618	90.0	427	8	ADT76864	Human pro
9	618	90.0	615	6	ABU99144	Novel hum
10	618	90.0	626	4	ABB778707	Human hig
11	618	90.0	644	4	ABG21101	Novel hum
12	618	90.0	644	5	ABB778710	Human hig
13	618	90.0	644	6	ABU99150	Novel hum
14	618	90.0	644	6	ABU99145	Novel hum
15	586	85.3	122	3	AAB37447	Human kin
16	585	85.2	435	4	ABG21105	Novel hum
17	556.5	81.0	117	2	AAR33350	Domaine 3
18	440	64.0	436	1	AAP40257	Bradykinin
19	413	60.1	434	1	AAP40633	Bradykinin
20	411	59.8	357	6	ABR41202	Human DTR
21	388	56.5	235	5	ABG60077	Human DTR
22	320.5	46.7	248	4	ABG21102	Novel hum
23	316	46.0	369	4	ABG21109	Novel hum
24	190	27.7	305	4	ABG21100	Novel hum
25	171.5	25.0	167	2	AAR98907	Mouse IMC

ALIGNMENTS

RESULT 1
AAY95426
ID AAY95426 standard; peptide; 123 AA.
XX
XX
AC
XX
DT
XX
DE Human high mol.wt. Kininogen domain 3.
XX
XX
XX
XX
XX
XX
XX
XX
OS Homo sapiens.
XX
XX
PN WO20035407-A2.
XX
XX
PD 22-JUN-2000.
XX
XX
PF 02-DEC-1999;
XX
PR 16-DEC-1998;
XX
PA (UTEM) UNIV TEMPLE.
PA (MCRAE R. K.
XX
PI Mcrae RK;
XX
DR WPI; 2000-442247/38.
XX
PT Composition for inhibiting angiogenesis and endothelial cell apoptosis and treating cancer, proliferating, inducing endothelial cell apoptosis and claimed domain 3 of human high mol.wt. kininogen analogs (HK). The invention relates to peptides (see AAY95405-24) that are analogues of certain sites in the HK domain 3, specifically Asn275-Lys82, Cys246-Cys249, Leu331-Tyr338 and Tyr339-Ser14. The peptides, in which native Cys residues may be replaced by Ala residues, inhibit endothelial cell proliferation and may also induce endothelial cell apoptosis. Compositions including the peptides are used in claimed methods for inhibiting angiogenesis, inhibiting endothelial cell apoptosis, Cancer, proliferation, and inducing endothelial cell apoptosis. Cancer,

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

1	618	90.0	123	3	AAY95426	Human hig
2	618	90.0	304	6	ABP70801	Human ext
3	618	90.0	322	6	ABP70799	Human ext
4	618	90.0	329	6	ABU9044	Human pro
5	618	90.0	358	6	ABP70800	Human ext
6	618	90.0	390	6	ABU99149	Novel hum
7	618	90.0	398	6	ABU99143	Novel hum
8	618	90.0	427	8	ADT76864	Human pro
9	618	90.0	615	6	ABU99144	Novel hum
10	618	90.0	626	4	ABB778707	Human hig
11	618	90.0	644	4	ABG21101	Novel hum
12	618	90.0	644	5	ABB778710	Human hig
13	618	90.0	644	6	ABU99150	Novel hum
14	618	90.0	644	6	ABU99145	Novel hum
15	586	85.3	122	3	AAB37447	Human kin
16	585	85.2	435	4	ABG21105	Novel hum
17	556.5	81.0	117	2	AAR33350	Domaine 3
18	440	64.0	436	1	AAP40257	Bradykinin
19	413	60.1	434	1	AAP40633	Bradykinin
20	411	59.8	357	6	ABR41202	Human DTR
21	388	56.5	235	5	ABG60077	Human DTR
22	320.5	46.7	248	4	ABG21102	Novel hum
23	316	46.0	369	4	ABG21109	Novel hum
24	190	27.7	305	4	ABG21100	Novel hum
25	171.5	25.0	167	2	AAR98907	Mouse IMC

CC rheumatoid arthritis, and ocular disorders characterized by undesired
XX vascularization of the retina are treated

Sequence 123 AA;	XX	SQ Sequence 304 AA;
Query Match 90.0%; Score 618; DB 3; Length 123; Best Local Similarity 100.0%; Pred. No. 5.5e-63; Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	Query Match 90.0%; Score 618; DB 6; Length 304; Best Local Similarity 100.0%; Pred. No. 1.9e-62; Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GKD FVQ PPT KIC VCG P R D I P T N S P L E T L T I K N A E N N A T F K I D N V K A R Q V V 62 Db 1 GKD FVQ PPT KIC VCG P R D I P T N S P L E T L T I K N A E N N A T F K I D N V K A R Q V V 60	QY 3 GKD FVQ PPT KIC VCG P R D I P T N S P L E T L T I K N A E N N A T F K I D N V K A R Q V V 62 Db 130 GKD FVQ PPT KIC VCG P R D I P T N S P L E T L T I K N A E N N A T F K I D N V K A R Q V V 189	
QY 63 AGK KYF IDP V A R E T T C S K E S N B E L T E C T K L G Q S L D C N A E V Y V W E K K I Y P T V 118 Db 61 AGK KYF IDP V A R E T T C S K E S N B E L T E C T K L G Q S L D C N A E V Y V W E K K I Y P T V 116	QY 63 AGK KYF IDP V A R E T T C S K E S N B E L T E C T K L G Q S L D C N A E V Y V W E K K I Y P T V 118 Db 190 AGK KYF IDP V A R E T T C S K E S N B E L T E C T K L G Q S L D C N A E V Y V W E K K I Y P T V 245	
RESULT 2 ABP70801 ID ABP70801 standard; protein; 304 AA. XX AC ABP70801; XX DT 26-AUG-2003 (first entry) XX DE Human extracellular messenger, EXMES-26. XX KW Human; extracellular messenger; EXMES; cytostatic; antidiabetic; KW immunosuppressive; autoimmune disorder; inflammatory disorder; diabetes; KW endocrine disorder; cancer. XX OS Homo sapiens. XX PN WO2003018612-A2. XX PD 06-MAR-2003. XX PF 22-AUG-2002; 2002WO-US027213. XX PR 24-AUG-2001; 2001US-0314811P. XX PR 14-DEC-2001; 2001US-0340549P. PR 18-JAN-2001; 2001US-0340584P. PR 18-JAN-2002; 2002US-0360595P. PR 11-MAR-2002; 2002US-0363432P. PR 15-MAR-2002; 2002US-0364677P. PR 05-APR-2002; 2002US-0370761P. PR 24-JUN-2002; 2002US-0391378P. XX PA (INCY-) INCYTE GENOMICS INC. XX DR Duggan BM, Lee S, Baughn MR, Hafalia AJA, Walia NK, Elliott VS, Elliott VS, PI Lee SY, Khare R, Wilson AD, Jin P, Hawkins PR, Tang YT, Burford N, PI Ding L, Yao MG, Becha SD, Tran UK, Chien D, Zebardadian Y, Lehr-Mason PM, PI Richardson TW, Kable AE, Chang H, Ramkumar J, PI PA WPI: 2003-278643/27. XX DR N-PSDB; ACC42388. XX PS Claim 1; Page 207; 224pp; English.	RESULT 3 ABP70799 ID ABP70799 standard; protein; 322 AA. XX AC ABP70799; XX DT 26-AUG-2003 (first entry) XX DE Human extracellular messenger, EXMES-26. XX KW Human; extracellular messenger; EXMES; cytostatic; antidiabetic; KW immunosuppressive; autoimmune disorder; inflammatory disorder; diabetes; KW endocrine disorder; cancer. XX OS Homo sapiens. XX PN WO2003018612-A2. XX PD 06-MAR-2003. XX PF 22-AUG-2002; 2002WO-US027213. XX PR 24-AUG-2001; 2001US-0314811P. XX PR 14-DEC-2001; 2001US-0340549P. PR 18-JAN-2002; 2002US-035055P. PR 11-MAR-2002; 2002US-0363432P. PR 15-MAR-2002; 2002US-0364677P. PR 05-APR-2002; 2002US-0370761P. PR 24-JUN-2002; 2002US-0391378P. XX PA (INCY-) INCYTE GENOMICS INC. XX DR Duggan BM, Lee S, Baughn MR, Hafalia AJA, Walia NK, Elliott VS, Elliott VS, PI Lee SY, Khare R, Wilson AD, Jin P, Hawkins PR, Tang YT, Burford N, PI Ding L, Yao MG, Becha SD, Tran UK, Chien D, Zebardadian Y, Lehr-Mason PM, PI Richardson TW, Kable AE, Chang H, Ramkumar J, PI PA WPI: 2003-278643/27. XX DR N-PSDB; ACC42388. XX PS The present invention relates to novel human extracellular messenger CC proteins (EXMES-1 to -28; ABP7074-ABP70801) and their coding sequences CC (ACC42361-ACC42388). The proteins are useful for preparing a composition CC for diagnosing or treating a disease or condition associated with decreased CC expression or overexpression of functional EXMES e.g. autoimmune CC auto-immune/inflammatory disorders, diabetes, endocrine disorders or CC cancer XX SQ Sequence 322 AA;	

Query Match 90.0%; Score 618; DB 6; Length 322;
 Best Local Similarity 100.0%; Pred. No. 2.1e-62; Gaps 0;
 Matches 116; Conservative 0; Indels 0; Gaps 0;

Qy 3 GKDVPQPCKICGCPDPTNSPEELTLTITKNAENNATFYKIDNPKKARYQV 62
 Db 148 GKDVPQPCKICGCPDPTNSPEELTLTITKNAENNATFYKIDNPKKARYQV 207
 Qy 63 AGKKYFIDVARETTCSKSNEEITESCETKLGQSLDNACTYVPMKKIYPTV 118
 Db 208 AGKKYFIDVARETTCSKSNEEITESCETKLGQSLDNACTYVPMKKIYPTV 263

RESULT 4
 ABU92044 standard; protein; 329 AA.
 XX
 AC ABU92044;
 XX DT 15-JUL-2003 (first entry)
 XX Human protein modification and maintenance molecule-24 (PMM-24).
 DE Human; protein modification and maintenance molecule; PMM; cancer; cell proliferation disorder; atherosclerosis; neurological disorder; epilepsy; Huntington's disease; stroke; immune disorder; allergy; inflammatory disorder; AIDS; developmental disorder; hypothyroidism; Cushing's syndrome; gastrointestinal disorder; epithelial disorder; infection; cytosatic; antiatherosclerotic; anticonvulsant; nootropic; neuroprotective; cerebroprotective; anti-HIV; antiallergic; vulnerability; antiinflammatory; thyromimetic.
 OS Homo sapiens.
 XX WO200301939-A2.
 XX PD 17-APR-2003.
 XX PF 11-OCT-2002; 2002WO-US032850.
 XX PR 12-OCT-2001; 2001US-0329689P.
 PR 25-OCT-2001; 2001US-0335703P.
 PR 09-NOV-2001; 2001US-0348887P.
 PR 28-NOV-2001; 2001US-0334145P.
 PR 06-DEC-2001; 2001US-0337451P.
 PR 14-DEC-2001; 2001US-0340584P.
 XX PA (INCY-) INCYTE GENOMICS INC.

XX Ramkumar J, Gorvad AE, Baughn MR, Emerling BM, Yang J, Lee SY; Tran UK, Becha SD, Dugan BM, Lee EA, Griffin JA, Li JX; Marquis JP, Yao MG, Richardson TW, Tang TY, Jin P, Chien D; Bhateria U, Burzili JD, Lee S, Blake JJ, Ho A, Zheng W; WPI: 2003-430274/40.
 DR N-PSDB; ACA92439.

XX New human protein modification and maintenance molecules (PMMM), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMM expression e.g. cancer, atherosclerosis, or infections.

Claim 1; Page 264-265; 311pp; English.

XX The present invention relates to the isolation of human protein modification and maintenance molecules (PMMM), and the polynucleotide sequences encoding them. A total of 40 PMMM polypeptides (designated PMM-1 to PMM-40) are disclosed. The sequences of the invention are useful for diagnosing a condition or disease associated with the expression of PMM in a subject, preparing a polyclonal or monoclonal antibody, and generating an expression profile of a sample containing the

CC polynucleotides. The diseases or conditions associated with decreased expression or overexpression of PMM are cell proliferation disorders (e.g. cancer, atherosclerosis), neurological disorders (e.g. AIDS, Huntington's disease, stroke), immune/inflammatory disorders, (e.g. AIDS, allergies), developmental disorders (e.g. hypothyroidism, Cushing's syndrome), gastrointestinal or epithelial disorders, and infections. The PMMM polypeptides or their fragments are useful in screening compounds for effectiveness as agonists or antagonists of the polypeptides, or in altering the expression of the target polynucleotide and compounds that specifically bind to, or modulate the activity of the polypeptide. ABU9221-ABU92060 represent the human PMMM polypeptides of the invention ABU9221-ABU92060 represent the human PMMM polypeptides of the invention

XX SQ Sequence 329 AA;

Query Match 90.0%; Score 618; DB 6; Length 329;
 Best Local Similarity 100.0%; Pred. No. 2.2e-62; Gaps 0; Gaps 0;
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GKDVPQPCKICGCPDPTNSPEELTLTITKNAENNATFYKIDNPKKARYQV 62
 Db 155 GKDVPQPCKICGCPDPTNSPEELTLTITKNAENNATFYKIDNPKKARYQV 214
 Qy 63 AGKKYFIDVARETTCSKSNEEITESCETKLGQSLDNACTYVPMKKIYPTV 118
 Db 215 AGKKYFIDVARETTCSKSNEEITESCETKLGQSLDNACTYVPMKKIYPTV 270
 RESULT 5
 ABP70800 ID ABP70800 standard; protein; 358 AA.
 XX AC ABP70800;
 XX DT 26-AUG-2003 (first entry)
 XX DE Human extracellular messenger, EXMES-27.
 XX KW Human; extracellular messenger; EXMES; cytosatic; antiidiabetic; immunosuppressive; autoimmune disorder; inflammatory disorder; diabetes;
 KW KW endocrine disorder; cancer.
 XX OS Homo sapiens.
 XX PN WO2003018612-A2.
 XX PR 06-MAR-2003.
 XX PD 06-MAR-2003.
 XX PR 22-AUG-2002; 2002WO-US027213.
 XX PA (INCY-) INCYTE GENOMICS INC.
 PR 24-AUG-2001; 2001US-0314811P.
 PR 14-DEC-2001; 2001US-0340584P.
 PR 18-JAN-2002; 2002US-0340595P.
 PR 11-MAR-2002; 2002US-0363432P.
 PR 15-MAR-2002; 2002US-0364607P.
 PR 05-APR-2002; 2002US-037612.
 PR 24-JUN-2002; 2002US-0391376P.
 XX PA (INCY-) INCYTE GENOMICS INC.
 PR 24-AUG-2001; 2001US-0314811P.
 PR 14-DEC-2001; 2001US-0340584P.
 PR 18-JAN-2002; 2002US-0340595P.
 PR 11-MAR-2002; 2002US-0363432P.
 PR 15-MAR-2002; 2002US-0364607P.
 PR 05-APR-2002; 2002US-037612.
 PR 24-JUN-2002; 2002US-0391376P.
 XX PA (INCY-) INCYTE GENOMICS INC.
 PR 24-AUG-2001; 2001US-0314811P.
 PR 14-DEC-2001; 2001US-0340584P.
 PR 18-JAN-2002; 2002US-0340595P.
 PR 11-MAR-2002; 2002US-0363432P.
 PR 15-MAR-2002; 2002US-0364607P.
 PR 05-APR-2002; 2002US-037612.
 PR 24-JUN-2002; 2002US-0391376P.
 XX PI Duggan BM, Lee S, Baughn MR, Hafalia AJA, Walia NK, Elliott VS, Lee SY, Khare R, Wilson AD, Hawkins PR, Tang YT, Burford N; PT PT preparing a composition for treating a disease associated with decreased expression or overexpression of functional EXMES e.g. autoimmune disorders or cancer.

PS Claim 1; Page 206; 224pp; English.

XX The present invention relates to novel human extracellular messenger proteins (EXMES-1 to -28; ABP7074-ABP7080) and their coding sequences (ACC42561-ACC42368). The proteins are useful for preparing a composition for diagnosing or treating a disease or condition associated with decreased expression or overexpression of functional EXMES e.g., autoimmune/inflammatory disorders, diabetes, endocrine disorders or cancer.

XX Sequence 358 AA;

Query Match 90.0%; Score 618; DB 6; Length 358;

Best Local Similarity 100.0%; Pred. No. 2.4e-62;

Matches 116; Conservative 0; Mismatches 0; Gaps 0;

Qy 3 GRDFVQPPTRKICVGCPRDPTNSPELETTLTHITKLNAENNATYFKIDNVKARVQV 62

Db 184 GRDFVQPPTRKICVGCPRDPTNSPELETTLTHITKLNAENNATYFKIDNVKARVQV 243

Qy 63 AGKKYFIDFVARETTCSKSNEELTESCTTKLGOSLDCNNAEVYYVPWEEKIYPTV 118

Db 244 AGKKYFIDFVARETTCSKSNEELTESCTTKLGOSLDCNNAEVYYVPWEEKIYPTV 299

RESULT 6

ABU99119 ID ABU99149 standard; protein; 390 AA.

XX DT 01-AUG-2003 (first entry)

XX Novel human GPCR related protein NOV12g.

XX Human; G-protein coupled receptor protein; GPCR related protein; DE

XX NOV; cytosstatic; cardiant; antiarteriosclerotic; antidiabetic; DE

XX immunomodulator; anti-HIV; antorectic; antiasthmatic; haemostatic; DE

XX anti-parkinsonian; neuroprotective; nootropic; gene therapy; vaccine; DE

XX NOVX-associated disorder; cardiomyopathy; atherosclerosis; cancer; DE

XX diabetes; immune disorder; AIDS; obesity; asthma; DE

XX haemopoietic disorder; Parkinson's disease; Alzheimer's disease; DE

XX infection; multiple sclerosis; cancer-associated cachexia; DE

XX wasting disorder; chronic disease; neurogenesis; cell differentiation; DE

XX chromosome mapping; haemopoiesis; wound healing; angiogenesis; DE

XX pharmacogenomic.

OS Homo sapiens.

XX WO200299116-A2.

XX PD 12-DEC-2002.

XX PF 04-JUN-2002; 2002WO-US017428.

XX PR 04-JUN-2001; 2001US-0295507P

PR 04-JUN-2001; 2001US-02955661P

PR 06-JUN-2001; 2001US-0295404P

PR 14-JUN-2001; 2001US-029541P

PR 15-JUN-2001; 2001US-029555P

PR 21-JUN-2001; 2001US-0295556P

PR 26-JUN-2001; 2001US-029549P

PR 13-AUG-2001; 2001US-0300883P

PR 13-AUG-2001; 2001US-0301550P

PR 27-AUG-2001; 2001US-0311972P

PR 29-AUG-2001; 2001US-0315071P

PR 04-SEP-2001; 2001US-0315660P

PR 17-SEP-2001; 2001US-0322293P

PR 14-OCT-2001; 2001US-03411862P

PR 28-FEB-2002; 2002US-0361189P

PR 12-MAR-2002; 2002US-0363673P

PR 12-MAR-2002; 2002US-0363676P

PR 03-JUN-2002; 2002US-00363676.

XX (CURA-) CURAGEN CORP.

XX Anderson DW, Baumgartner JC, Boldog FL, Casman SJ, Edinger SR, Ganguli EA, Gerlach VL, Gorman L, Guo X, Hjalt T, Kekuda R, Li L, Mardougal JR, Malyanikar UM, Millet I, Padigaru M, Paturajan M, Pena CEA, Rastelli L, Shimkets RA, Stone DJ, Spytek KA, Vernet CAM, Voss EZ, Zerhusen BD;

XX DR WPI; 2003-140627/13.

XX DR N-PSDB; ACD03653.

XX New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or pharmacogenomics.

XX PS Claim 1; Page 147; 332pp; English.

XX The invention describes an isolated polypeptide (I) comprising any of 27 CC residue amino acid sequences, given in the specification, a CC mature form of them, a sequence that is at least 95 % identical to them, or a sequence having one or more conservative substitutions in them. The CC polypeptide is useful in manufacturing a medicament for treating a CC syndrome associated with a human disease selected from a pathology CC associated with the polypeptide. The NOVX polypeptides, polymucleptides CC and antibodies are useful in treating or preventing NOVX-associated CC disorders, e.g. cardiomyopathy, atherosclerosis, cancer, diabetes, immune CC disease, AIDS, obesity, asthma, haemopoietic disorders, Parkinson's CC disease, Alzheimer's disease, infections, multiple sclerosis, cancer- CC associated cachexia, and other wasting disorders associated with chronic CC diseases. The nucleic acids and polypeptides may also be used as targets CC for the identification of small molecules that modulate or inhibit e.g. CC neurogenesis, cell differentiation, cell proliferation, haematopoiesis, CC wound healing and angiogenesis, in gene therapy, in generation of CC therapeutic or diagnostic methods. The nucleic acids are further used as CC hybridisation probes, in chromosome mapping, tissue typing, preventive CC medicine and pharmacogenomics. The polypeptides are also useful as CC vaccines. This is the amino acid sequence of a novel human G-protein CC coupled receptor related protein NOVX.

XX SQ Sequence 390 AA;

Query Match 90.0%; Score 618; DB 6; Length 390;

Best Local Similarity 100.0%; Pred. No. 2.7e-62;

Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GRDFVQPPTRKICVGCPRDPTNSPELETTLTHITKLNAENNATYFKIDNVKARVQV 62

Db 216 GRDFVQPPTRKICVGCPRDPTNSPELETTLTHITKLNAENNATYFKIDNVKARVQV 275

Qy 63 AGKKYFIDFVARETTCSKSNEELTESCTTKLGOSLDCNNAEVYYVPWEEKIYPTV 118

Db 276 AGKKYFIDFVARETTCSKSNEELTESCTTKLGOSLDCNNAEVYYVPWEEKIYPTV 331

RESULT 7

ABU99143 ID ABU99143 standard; protein; 398 AA.

XX AC ABU99143;

XX DT 01-AUG-2003 (first entry)

XX Novel human GPCR related protein NOV12a.

XX Human; G-protein coupled receptor related protein; GPCR related protein; NOV; cytosstatic; cardiant; antiarteriosclerotic; antidiabetic; DE

XX immunomodulator; anti-HIV; antorectic; antiasthmatic; haemostatic; DE

XX anti-parkinsonian; neuroprotective; nootropic; gene therapy; vaccine; DE

XX NOVX-associated disorder; cardiomyopathy; atherosclerosis; cancer; DE

XX diabetes; immune disorder; AIDS; obesity; asthma; DE

XX haemopoietic disorder; Parkinson's disease; Alzheimer's disease; DE

XX infection; multiple sclerosis; cancer-associated cachexia; DE

XX wasting disorder; chronic disease; neurogenesis; cell differentiation; DE

XX chromosome mapping; haemopoiesis; wound healing; angiogenesis; DE

XX pharmacogenomic.

KW diabetes; immune disorder; AIDS; obesity; asthma;
 KW haemopoietic disorder; Parkinson's disease; Alzheimer's disease;
 KW infection; multiple sclerosis; cancer-associated cachexia;
 KW wasting disorder; chronic disease; neurogenesis; cell differentiation;
 KW cell proliferation; haemopoiesis; wound healing; angiogenesis;
 KW chromosome mapping; tissue typing; preventive medicine; pharmacogenomic.
 OS Homo sapiens.
 PN WO200299116-A2.
 PD 12-DEC-2002.
 XX PF 04-JUN-2002; 2002NO-US017428.
 XX PR 04-JUN-2001; 2001US-0295607P.
 PR 04-JUN-2001; 2001US-0295661P.
 PR 06-JUN-2001; 2001US-0295404P.
 PR 06-JUN-2001; 2001US-0295418P.
 PR 14-JUN-2001; 2001US-0295285P.
 PR 15-JUN-2001; 2001US-0295556P.
 PR 21-JUN-2001; 2001US-0295949P.
 PR 26-JUN-2001; 2001US-0300883P.
 PR 28-JUN-2001; 2001US-0301550P.
 PR 13-AUG-2001; 2001US-0311172P.
 PR 29-AUG-2001; 2001US-0311071P.
 PR 14-SEP-2001; 2001US-0315660P.
 PR 17-OCT-2001; 2001US-0322293P.
 PR 14-DEC-2001; 2001US-0322106P.
 PR 28-FEB-2002; 2002US-0361186P.
 PR 12-MAR-2002; 2002US-0363173P.
 PR 12-MAR-2002; 2002US-0363676P.
 PR 03-JUN-2002; 2002US-00363676.
 PA (CURA-) CURAGEN CORP.
 XX PI Anderson DW, Baumgartner JC, Boldog FL, Casman SJ, Edinger SR; Li L; Guo X, Halt T, Kekuda R, Padigaru M, Paturajan M; Vernet CAM; Pena CE, Rastelli L, Shirkets RA, Stone DJ, Spytek KP, Voss EZ, Zerhusen BD; DR 2003-140627/13; N-PSDB; ACD03647.
 XX PT New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or pharmacogenomics.
 XX PS Claim 1; Page 143; 332PP; English.
 XX The invention describes an isolated polypeptide (I) comprising any of 27 118-361 residue amino acid sequences, given in the specification, a mature form of them, a sequence that is at least 95 % identical to them, or a sequence having one or more conservative substitutions in them. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease selected from a pathology associated with the polypeptide. The NOVX polypeptides, polynucleotides and antibodies are useful in treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, atherosclerosis, cancer, diabetes, immune disorders, AIDS, obesity, asthma, haematopoietic disorders, Parkinson's disease, Alzheimer's disease, infections, multiple sclerosis, cancer-associated cachexia, and other wasting disorders associated with chronic diseases. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haematopoiesis, wound healing and angiogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or diagnostic methods. The nucleic acids are further used as hybridisation probes in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The polypeptides are also useful as vaccines. This is the amino acid sequence of a novel human G-protein coupled receptor related protein NOV
 CC CC
 XX Sequence 398 AA;
 XX Best Local Similarity 100.0%; Pred. No. 2.8e-62;
 Matches 116; Conservative 0; Mis-matches 0; Indels 0; Gaps 0;
 Qy 3 GKDFVQPPTKICVGCRDIPNSPEELTTIKLNAAANNATYFKIDNVKKARQVV 62
 Db 224 GKDFVQPPTKICVGCRDIPNSPEELTTIKLNAAANNATYFKIDNVKKARQVV 283
 Qy 63 AGKRYFIDFVARETTSKESNEBELTSCETKLGQSLDCNAEVYYVPWEKKIYPTV 118
 Db 284 AGKRYFIDFVARETTSKESNEBELTSCETKLGQSLDCNAEVYYVPWEKKIYPTV 339
 RESULT 8
 ID ADE76864 standard; protein; 427 AA.
 XX ADE76864;
 XX XX
 AC XX
 AC XX
 DT 29-JAN-2004 (first entry)
 DE Human protein expressed in a liver disorder #9.
 XX XX
 KW human; liver disorder; hyperlipidaemia; hypertension; type II diabetes;
 KW tumour; liver; inflammatory disorder; immune response disorder;
 KW high-throughput screening; differential gene expression; gene therapy.
 XX XX
 KW Homo sapiens.
 OS XX
 XX US2003108871-A1.
 XX XX
 PD 12-JUN-2003.
 XX XX
 PF 30-JUL-2001; 2001US-00919039.
 XX XX
 PR 28-JUL-2000; 2000US-0222213P.
 PA (KASE/) KASER M. R.
 PA XX
 PI Kaser MR;
 XX XX
 DR WPI; 2004-031227/03.
 DR N-PSDB; ADE76863.
 XX PT Composition comprising several cDNAs that are differentially expressed in treated human C3A liver cell cultures, useful for treating liver disorders.
 XX XX
 PA Claim 1; SEQ ID NO 29; 41PP; English.
 XX XX
 CC The invention relates to a composition comprising several cDNAs that are differentially expressed in a liver disorder. The composition is useful for treating liver disorder such as hyperlipidaemia, hypertension, type II diabetes, tumours of the liver and disorders of the inflammatory and immune response. The composition is useful for a high-throughput method of screening several molecules or compounds to identify a ligand which specifically binds a cDNA. A protein encoded by the cDNA is useful for a high-throughput method for using a protein to screen several molecules or compounds to identify at least one ligand which specifically binds the protein which involves combining the protein encoded by the cDNA with several of molecules or compounds under conditions to allow specific binding, and detecting specific binding between the protein and a molecule or compound, therefore identifying a ligand which specifically binds the protein. The composition is useful in gene therapy, to quantifying differential gene expression, can be used in gene therapy, to formulate prognosis and to design a treatment regimen and to monitor the efficacy of treatment. The present sequence represents the amino acid sequence of a protein encoded by a cDNA differentially expressed in a

PI	Voss EZ,	Zerhusen BD;
XX	XX	
SQ	Sequence 427 AA.	
Query Match	90.0%;	Score 618; DB 8; Length 427;
Best Local Similarity	100.0%;	Pred. No. 3.1e-62;
Matches 116;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
Qy	3 GKDFFVQPTKICVGCPDRDIPNSPELEETLTHITKLNAENNATFYFKIDNVKKARVVY 62	
Db	253 GKDFFVQPTKICVGCPDRDIPNSPELEETLTHITKLNAENNATFYFKIDNVKKARVVY 312	
RESUL T 9		
ID ABU99144	ABU99144 standard; protein; 615 AA.	
XX	XX	
AC ABU99144;		
CC		
DR 01-AUG-2003 (first entry)		
XX		
Novel human GPCR related protein NOV12b.		
XX		
KW Human; G-protein coupled receptor related protein; GPCR related protein;		
KW NOV; cytosolic; cardiotropic; antiarachidonic; anti-diabetic;		
KW immunomodulator; anti-HIV; aborectic; antiasthmatic; haemostatic;		
KW antiparkinsonian; neuroprotective; nootropic; gene therapy; vaccine;		
KW NOVX-associated disorder; cardiomyopathy; atherosclerosis; cancer;		
KW diabetes; immune disorder; AIDS; obesity; asthma;		
KW haematopoietic disorder; Parkinson's disease; Alzheimer's disease;		
KW infection; multiple sclerosis; cancer-associated cachexia; disease;		
KW wasting disorder; chronic disease; neurogenesis; cell differentiation;		
KW chromosome mapping; tissue typing; preventive medicine; pharmacogenomic.		
Homo sapiens.		
XX		
PN WO200299116-A2.		
XX		
PD 12-DEC-2002.		
XX		
PR 04-JUN-2002; 2002WO-US017428.		
XX		
PR 04-JUN-2001; 2001US-0295607P.		
PR 06-JUN-2001; 2001US-0295610P.		
PR 06-JUN-2001; 2001US-0295614P.		
PR 14-JUN-2001; 2001US-0295218P.		
PR 15-JUN-2001; 2001US-0298556P.		
PR 21-JUN-2001; 2001US-0299349P.		
PR 26-JUN-2001; 2001US-0299831P.		
PR 28-JUN-2001; 2001US-0301550P.		
PR 13-AUG-2001; 2001US-0311972P.		
PR 27-AUG-2001; 2001US-0315071P.		
PR 29-AUG-2001; 2001US-0315660P.		
PR 14-SEP-2001; 2001US-0322293P.		
PR 17-SEP-2001; 2001US-0322706P.		
PR 14-DEC-2001; 2001US-0341186P.		
PR 28-DEC-2002; 2002US-0361189P.		
PR 12-MAR-2002; 2002US-0363673P.		
PR 12-MAR-2002; 2002US-0363676P.		
PR 03-JUN-2002; 2002US-00363676.		
XX		
PA (CURA-) CURAGEN CORP.		
XX		
Anderson DW, Baumgartner JC, Boldog FL, Casman SJ, Edinger SR, Garschall EA, Gerlach WI, Gorman L, Guo X, Hjalt T, Kekuda R, Li L, Macdougall JR, Malayan VK, Millet I, Padigaru M, Paturajan M, Shinketsu RA, Rastelli L, Srinivasan I, Stone DJ, Syprett KA, Vernet CAM, PN CEA, PA	Location/Qualifiers	
XX	Key Domains	
PI 384. 503 /label= D5_domain		
DR 18-JUL-2002 (first entry)		
PR RESULT 10		
XX		
AC ABB78707;		
XX		
DT 18-JUL-2002 (first entry)		
XX		
DE Human high molecular weight kininogen (HK) mature protein SEQ ID NO:1.		
XX		
AC ABB78707;		
XX		
DE Human; kininogen; high molecular weight kininogen; HK; D5 domain; DS receptor; angiogenesis; endothelial cell; cycostatic; antitumour; ophthalmological; gynaecological; antidiabetic; antilulcer; thromolytic; antiangiogenic; apoptosis; gene therapy.		
XX		
OS Homo sapiens.		
XX		
PN Key Domains		
XX		
PN WO200214369-A2 /label= D5_domain		

XX		WO200175067-A2.
PD	PN	XX
XX	XX	11-OCT-2001.
PP	PR	XX
PR	XX	30-MAR-2001; 2001WO-US008631.
XX	XX	XX
(ATE-)	ATTENON LLC.	PR 31-MAR-2000; 2000US-00540217.
PA	XX	PR 23-AUG-2000; 2000US-00649167.
PI	XX	PA (HYSE-) HYSEQ INC.
XX	XX	XX
DR	WPI; 2002-393611/42.	PI Drmanac RT, Liu C, Tang YT;
XX	PT Novel human kininogen D5 domain polypeptides useful for treating	XX
PT	conditions associated with endothelial cell migration, proliferation,	XX
PT	invasion or angiogenesis, e.g. arthritis, macular degeneration, benign	XX
PT	hyperplasia.	XX
PS	Disclosure: Page 13; 8app; English.	XX
XX	The present invention describes an isolated polypeptide (I) that corresponds to the D5 domain of human kininogen, or biologically active peptide fragment, homologe or functional derivative, and which: (a) inhibits angiogenesis; (b) binds to the D5 binding site on endothelial cells (EC); (c) activates signalling pathways leading to the introduction of apoptosis; and/or (d) inhibits the signalling pathway required for maintenance of EC viability. (I) has cyrostatic, antitumour, antiatherosclerotic, vasotropis, vunlear, tranquiliser, thrombolytic, ophthalmological, gynaecological, antiulcer, antidiabetic, antiarthritic, antiangiogenic, antiapoptotic and endocrine activities. An antibody (IX), specific for an epitope of (I), is useful for inhibiting tumour growth or angiogenesis in a subject. (I), a D5 fusion polypeptide (III) or a dimeric or trimeric fusion polypeptide (III) can be used for inhibiting EC migration, proliferation, invasion, or angiogenesis, or for inducing EC apoptosis. An angiogenic EC-targeting pharmaceutical composition comprising (I), (II), or (III), can be used for treating a subject having a disease or condition associated with undesired EC migration, proliferation, invasion or angiogenesis. (I), (II), or (III) can be used for isolating a D5 domain binding molecule from a complex mixture and for isolating or enriching cells expressing D5 domain binding sites from a cell mixture. The present sequence represents the mature human high molecular weight kininogen (HK) protein, which is given in the exemplification of the present invention.	XX
XX	Sequence 626 AA;	XX
SQ	Query Match 90.0%; Score 618; DB 5; Length 626;	XX
	Best Local Similarity 100.0%; Pred. No. 5.3e-62;	XX
	Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX
Qy	3 GKDFFQPPTKICVGCPRDPTNSPELETHTITKLNAENNATYFKIDDNVKKARQVY 62	XX
Db	235 GKDFFQPPTKICVGCPRDPTNSPELETHTITKLNAENNATYFKIDDNVKKARQVY 294	XX
Qy	63 AGKKYFIDFVARETTCSKEEELTSCEFKLGSQSLDCAEVYVPPWEKKIYPTV 118	XX
Db	295 AGKKYFIDFVARETTCSKEEELTSCEFKLGSQSLDCAEVYVPPWEKKIYPTV 350	XX
SQ	Sequence 626 AA;	XX
Qy	90.0%; Score 618; DB 4; Length 644;	XX
	Best Local Similarity 100.0%; Pred. No. 5.5e-62;	XX
	Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX
Qy	3 GKDFFQPPTKICVGCPRDPTNSPELETHTITKLNAENNATYFKIDDNVKKARQVY 62	XX
Db	253 GKDFFQPPTKICVGCPRDPTNSPELETHTITKLNAENNATYFKIDDNVKKARQVY 312	XX
Qy	63 AGKKYFIDFVARETTCSKEEELTSCEFKLGSQSLDCAEVYVPPWEKKIYPTV 118	XX
Db	313 AGKKYFIDFVARETTCSKEEELTSCEFKLGSQSLDCAEVYVPPWEKKIYPTV 368	XX
RESULT 11		
XX	ABG21101 standard; protein; 644 AA.	
XX	ID ABG21101	RESULT 12
AC	ABG21101;	ABB7810
XX	18-FEB-2002 (first entry)	ID ABB7810 standard; protein; 644 AA.
DT	18-FEB-2002 (first entry)	XX
XX	Novel human diagnostic protein #21092.	DE Human high molecular weight kininogen (HK) protein.
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.	XX DE Human; kininogen; high molecular weight kininogen; HK; D5 domain; D5 receptor; angiogenesis; endothelial cell; cytostatic; antitumor; KW Homo sapiens

Score 618; DB 5; Length 644;
Query Match 90.0%; **Pred.** No. 5.e-62;
Best Local Similarity 100.0%;
Conservative matches 16; **Conservative matches** 0;
Mismatches 0; **Indels** 0;
Gaps 0;

DR N-PSDB; ACD03654.
 XX
 PT New NOVX polypeptides and nucleic acids, useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancers, cardionyopathy,
 PT

PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or pharmacogenomics.

PT XX Claim 1; Page 148; 332pp; English.

XX The invention describes an isolated polypeptide (I) comprising any of 27 CC 118-961 residue amino acid sequences, given in the specification, a mature form of them, a sequence that is at least 95 % identical to them, or a sequence having one or more conservative substitutions in them. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease selected from a pathology associated with the polypeptide. The NOVX polypeptides, Polynucleotides and antibodies are useful in treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, atherosclerosis, cancer, diabetes, immune disorders, AIDS, obesity, asthma, haematopoietic disorders, Parkinson's disease, Alzheimer's disease, infections, multiple sclerosis, cancer-associated cachexia, and other wasting disorders associated with chronic diseases. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haemopoiesis, wound healing, and angiogenesis, in gene therapy, in generation of therapeutic or diagnostic methods. The nucleic acids are further used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The polypeptides are also useful as vaccines. This is the amino acid sequence of a novel human G-protein coupled receptor related protein NOV

XX Sequence 644 AA;

Query Match Score 618; DB 6; Length 644;
Best Local Similarity 100.0%; Pred. No. 5_5e-62;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GKDFFQPPTKICVGCPDRDIPNSPLEETLTTITKLNAENNATFYFKIDNVKARVQV 62
Db 253 GKDFFQPPTKICVGCPDRDIPNSPLEETLTTITKLNAENNATFYFKIDNVKARVQV 312

Qy 63 AGKKYFIDFVARETCSKESNEELTESCETKKGOSLDCAENAYYVPMKKIYPTV 118
Db 313 AGKKYFIDFVARETCSKESNEELTESCETKKGOSLDCAENAYYVPMKKIYPTV 368

RESULT 14

ABU99145

ID ABU99145 standard; protein; 644 AA.

XX AC ABU99145;

XX DT 01-AUG-2003 (first entry)

XX Novel human GPCR related protein NOV12C.

XX Human G-protein coupled receptor related protein; GPCR related protein; KW NOV; cyrostatic; cardiant; antiarrhythmic; antidiabetic; KW immunomodulator; anti-HIV; anorectic; antiasthmatic; haemostatic; KW antiparkinsonian; neuroprotective; nonotropic; gene therapy; vaccine; KW NOVX-associated disorder; cardiomyopathy; atherosclerosis; cancer; KW diabetes; immune disorder; AIDS; obesity; asthma; KW haematopoietic disorder; Parkinson's disease; Alzheimer's disease; KW infection; multiple sclerosis; cancer-associated cachexia; KW wasting disorder; chronic disease; neurogenesis; cell differentiation; KW chromosome mapping; tissue typing; preventive medicine; pharmacogenomic. KW Homo sapiens.

XX OS WO20029116-A2.

XX PD 12-DEC-2002.

XX PF 04-JUN-2002; 2002WO-US017428.

XX

PR 04-JUN-2001; 2001US-0295607P.
PR 04-JUN-2001; 2001US-0295611P.
PR 06-JUN-2001; 2001US-0296414P.
PR 06-JUN-2001; 2001US-0296418P.
PR 14-JUN-2001; 2001US-0298255P.
PR 15-JUN-2001; 2001US-029856P.
PR 21-JUN-2001; 2001US-039941P.
PR 26-JUN-2001; 2001US-030083P.
PR 28-JUN-2001; 2001US-030150P.
PR 13-AUG-2001; 2001US-031192P.
PR 27-AUG-2001; 2001US-031071P.
PR 29-AUG-2001; 2001US-031566P.
PR 14-SEP-2001; 2001US-0322233P.
PR 17-SEP-2001; 2001US-032706P.
PR 14-DEC-2001; 2001US-034116P.
PR 28-FEB-2002; 2002US-036119P.
PR 12-MAR-2002; 2002US-036313P.
PR 12-MAR-2002; 2002US-0363676P.
PR 03-JUN-2002; 2002US-00363676.
XX (CURA-) CURAGEN CORP.

PA XX DR N-PSDB; ACD3649.

XX Anderson DW, Baumgartner JC, Boldog FL, Casman SJ, Edinger SR, Gangolli EA, Geslach VL, Gorman L, Guo X, Hjalt T, Kekida R, Li L; PT Macdougall JR, Malyankar UM, Millet I, Padigaru M, Pattrajan M; PT Pena CEA, Pastelle L, Shimkets RA, Stone DJ, Spyte KA, Vernet CAM; PT Voss EZ, Zerhusen BD; XX DR WPI; 2003-140627/13.
XX DR N-PSDB; ACD3649.

XX New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, tissue typing or pharmacogenomics.

XX Claim 1; Page 144-145; 332pp; English.

XX The invention describes an isolated polypeptide (I) comprising any of 27 CC 118-961 residue amino acid sequences, given in the specification, a mature form of them, a sequence that is at least 95 % identical to them, or a sequence having one or more conservative substitutions in them. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease selected from a pathology associated with the polypeptide. The NOVX polypeptides, Polynucleotides and antibodies are useful in treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, atherosclerosis, cancer, diabetes, immune disease, AIDS, obesity, asthma, haematopoietic disorders, Parkinson's disease, Alzheimer's disease, infections, multiple sclerosis, cancer-associated cachexia, and other wasting disorders associated with chronic diseases. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g., neurogenesis, cell differentiation, cell proliferation, hematopoiesis, wound healing and angiogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or diagnostic methods. The nucleic acids are further used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The polypeptides are also useful as vaccines. This is the amino acid sequence of a novel human G-protein coupled receptor related protein NOV

XX Sequence 644 AA;

XX Query Match Score 90.0%; Score 618; DB 6; Length 644;
Best Local Similarity 100.0%; Pred. No. 5_5e-62;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GKDFFQPPTKICVGCPDRDIPNSPLEETLTTITKLNAENNATFYFKIDNVKARVQV 62
Db 253 GKDFFQPPTKICVGCPDRDIPNSPLEETLTTITKLNAENNATFYFKIDNVKARVQV 312

Qy 63 AGKKYFIDFVARETCSKESNEELTESCETKKGOSLDCAENAYYVPMKKIYPTV 118
Db 313 AGKKYFIDFVARETCSKESNEELTESCETKKGOSLDCAENAYYVPMKKIYPTV 368

XX RESULT 14

XX ABU99145

XX ID ABU99145 standard; protein; 644 AA.

XX DE 01-AUG-2003 (first entry)

XX Novel human GPCR related protein NOV12C.

XX Human G-protein coupled receptor related protein; GPCR related protein; KW NOV; cyrostatic; cardiant; antiarrhythmic; antidiabetic; KW immunomodulator; anti-HIV; anorectic; antiasthmatic; haemostatic; KW antiparkinsonian; neuroprotective; nonotropic; gene therapy; vaccine; KW NOVX-associated disorder; cardiomyopathy; atherosclerosis; cancer; KW diabetes; immune disorder; AIDS; obesity; asthma; KW haematopoietic disorder; Parkinson's disease; Alzheimer's disease; KW infection; multiple sclerosis; cancer-associated cachexia; KW wasting disorder; chronic disease; neurogenesis; cell differentiation; KW chromosome mapping; tissue typing; preventive medicine; pharmacogenomic. KW Homo sapiens.

XX OS WO20029116-A2.

XX PD 12-DEC-2002.

XX PF 04-JUN-2002; 2002WO-US017428.

XX

Query Match Score 90.0%; Score 618; DB 6; Length 644;
Best Local Similarity 100.0%; Pred. No. 5.5e-62;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GKDFFQPPTKICVGCPDRDIPNSPLEETLTTITKLNAENNATFYFKIDNVKARVQV 62
Db 253 GKDFFQPPTKICVGCPDRDIPNSPLEETLTTITKLNAENNATFYFKIDNVKARVQV 312

Qy 63 AGKKYFIDFVARETCSKESNEELTESCETKKGOSLDCAENAYYVPMKKIYPTV 118

Db 313 AGKKYFIDFVARETTCSKESNEELTESCTKLGQSLDNCNAEVTVVPWEKKIYPTV 368

RESULT 15

AAB37447
ID AAB37447 standard; protein; 122 AA.

XX

AC

AAB37447;

XX

DT

21-FEB-2001 (first entry)

XX

DE

Human kininogen D3.

XX

KW

Enzyme; legumain; endopeptidase; cystatin; human; kininogen.

XX

OS

Homo sapiens.

XX

PN

W0200064945-A1.

XX

PD

02-NOV-2000.

XX

PP

20-APR-2000; 2000WO-GB001571.

XX

PR

22-APR-1999;

99GB-000009133.

XX

PA

(BABR-)

BABRAHAM INST.

XX

PI

Abrahamsen M,

Barrett AJ;

XX

DR

2000-687316/67.

XX

PT

Inhibition of mammalian legumain or legumain-related endopeptidase by

PT

cystatin involves interaction with second papain-non-reactive site of

PT

cystatin.

XX

PS

Disclosure: Fig 4; 45pp; English.

XX

CC

The present invention relates to inhibition of the enzymatic activity of

CC

legumain or a legumain-related endopeptidase by cystatin. The inhibition

CC

involves an interaction between legumain and a papain-non-reactive site

CC

of cystatin. Legumain (EC 3.4.22.34) is a cysteine endopeptidase, and

CC

performs a protein processing function. The present sequence is human

CC

kininogen D3, which was used in the present invention. Kininogen is a

CC

type 3 cystatin

XX

SQ

Sequence 122 AA:

Query Match Similarity 85.3%; Score 586; DB 3; Length 122;
Best Local Similarity 100.0%; Pred. No. 2,7e-59; Indels 0; Gaps 0;
Matches 110; Conservative 0; Mismatches 0;

Qy 9 PPTKICVGCPRDIPNTSPELBTLLTITKINAENNATPFKIDNVKKARVQVYAGKVF 68

Db 1 PPTKICVGCPRDIPNTSPELBTLLTITKINAENNATPFKIDNVKKARVQVYAGKVF 60

Qy 69 IDFVARETTCSKESNEELTESCTKLGQSLDNCNAEVTVVPWEKKIYPTV 118

Db 61 IDFVARETTCSKESNEELTESCTKLGQSLDNCNAEVTVVPWEKKIYPTV 110

Search completed: September 24, 2004, 14:08:38
Job time : 52.308 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 24, 2004, 14:07:01 ; Search time 14.732 Seconds
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Title: US-10-661-784-3

Perfect score: 687

Sequence: 1 GSGKDFVQPPKIKVGCPRD.....VPWEEKIYPTVTNHWCEF 127

Scoring table: BLOSUM62

GapOp 10.0 , GapExt 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:

389414

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
 1: /cggn_6/prodata/2/iaa/5A_COMB.pep.*
 2: /cggn_6/prodata/2/iaa/5B_COMB.pep.*
 3: /cggn_6/prodata/2/iaa/6A_COMB.pep.*
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 5: /cggn_6/prodata/2/iaa/pcrtus_COMB.pep.*
 6: /cggn_2/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	558	81.2	117	1 US-08-193-114B-1	Sequence 1, Appli
2	556.5	81.0	117	5 PCT-US20-06109-1	Sequence 1, Appli
3	163.5	23.8	145	2 US-08-832-535-2	Sequence 2, Appli
4	163.5	23.8	145	3 US-09-019-485-5	Sequence 3, Appli
5	163.5	23.8	145	3 US-09-431-180-9	Sequence 9, Appli
6	163.5	23.8	145	3 US-09-617-302-9	Sequence 2, Appli
7	163.5	23.8	145	4 US-09-528-416B-2	Sequence 2, Appli
8	163.5	23.8	178	2 US-08-191-522-1	Sequence 1, Appli
9	163	23.7	178	3 US-09-114-777-1	Sequence 1, Appli
10	138.5	20.2	121	4 US-09-77-932-14	Sequence 14, Appli
11	138.5	20.2	128	4 US-09-775-932-12	Sequence 12, Appli
12	138.5	20.2	149	4 US-08-461-010C-2	Sequence 2, Appli
13	138.5	20.2	149	3 US-08-744-138-2	Sequence 2, Appli
14	138.5	20.2	149	3 US-09-431-480-8	Sequence 8, Appli
15	138.5	20.2	149	3 US-09-431-480-10	Sequence 10, Appli
16	138.5	20.2	149	3 US-09-617-302-8	Sequence 8, Appli
17	138.5	20.2	149	3 US-09-617-302-10	Sequence 10, Appli
18	138.5	20.2	149	4 US-09-241-316-2	Sequence 2, Appli
19	138.5	20.2	149	4 US-09-940-497-2	Sequence 2, Appli
20	138.5	20.2	149	4 US-09-849-303-16	Sequence 16, Appli
21	137.5	20.0	112	4 US-09-775-932-24	Sequence 24, Appli
22	136.5	19.9	118	4 US-09-775-932-24	Sequence 24, Appli
23	135.5	19.7	146	6 P432264-6	Patent No. 5432264
24	134	19.5	148	5 PCT-US5-07135-2	Sequence 2, Appli
25	132.5	19.3	120	4 US-09-775-932-2	Sequence 2, Appli
26	132.5	19.3	145	2 US-08-332-535-11	Sequence 11, Appli
27	132.5	19.3	146	2 US-08-791-522-3	Sequence 3, Appli

Sequence 3, Appli

Sequence 4, Appli

Sequence 5, Appli

Sequence 6, Appli

Sequence 7, Appli

Sequence 8, Appli

Sequence 9, Appli

Sequence 10, Appli

Sequence 11, Appli

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Sequence 49, Appli

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Sequence 51, Appli

Sequence 52, Appli

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Sequence 76, Appli

Sequence 77, Appli

Sequence 78, Appli

Sequence 79, Appli

Sequence 80, Appli

Sequence 81, Appli

Sequence 82, Appli

Sequence 83, Appli

Sequence 84, Appli

Sequence 85, Appli

Sequence 86, Appli

Sequence 87, Appli

Sequence 88, Appli

Sequence 89, Appli

Sequence 90, Appli

Sequence 91, Appli

Sequence 92, Appli

Sequence 93, Appli

Sequence 94, Appli

Sequence 95, Appli

Sequence 96, Appli

Sequence 97, Appli

Sequence 98, Appli

Sequence 99, Appli

Sequence 100, Appli

Sequence 101, Appli

Sequence 102, Appli

Sequence 103, Appli

Sequence 104, Appli

Sequence 105, Appli

Sequence 106, Appli

Sequence 107, Appli

Sequence 108, Appli

Sequence 109, Appli

Sequence 110, Appli

Sequence 111, Appli

Sequence 112, Appli

Sequence 113, Appli

Sequence 114, Appli

Sequence 115, Appli

Sequence 116, Appli

Sequence 117, Appli

Sequence 118, Appli

Sequence 119, Appli

Sequence 120, Appli

Sequence 121, Appli

Sequence 122, Appli

Sequence 123, Appli

Sequence 124, Appli

Sequence 125, Appli

Sequence 126, Appli

Sequence 127, Appli

Sequence 128, Appli

Sequence 129, Appli

Sequence 130, Appli

Sequence 131, Appli

Sequence 132, Appli

Sequence 133, Appli

Sequence 134, Appli

Sequence 135, Appli

Sequence 136, Appli

Sequence 137, Appli

Sequence 138, Appli

Sequence 139, Appli

Sequence 140, Appli

Sequence 141, Appli

Sequence 142, Appli

Sequence 143, Appli

Sequence 144, Appli

Sequence 145, Appli

Sequence 146, Appli

Sequence 147, Appli

Sequence 148, Appli

Sequence 149, Appli

Sequence 150, Appli

Sequence 151, Appli

Sequence 152, Appli

Sequence 153, Appli

Sequence 154, Appli

Sequence 155, Appli

Sequence 156, Appli

Sequence 157, Appli

Sequence 158, Appli

Sequence 159, Appli

Sequence 160, Appli

Sequence 161, Appli

Sequence 162, Appli

Sequence 163, Appli

Sequence 164, Appli

Sequence 165, Appli

Sequence 166, Appli

Sequence 167, Appli

Sequence 168, Appli

Sequence 169, Appli

Sequence 170, Appli

Sequence 171, Appli

Sequence 172, Appli

Sequence 173, Appli

Sequence 174, Appli

Sequence 175, Appli

Sequence 176, Appli

Sequence 177, Appli

Sequence 178, Appli

Sequence 179, Appli

Sequence 180, Appli

Sequence 181, Appli

Sequence 182, Appli

Sequence 183, Appli

Sequence 184, Appli

Sequence 185, Appli

Sequence 186, Appli

Sequence 187, Appli

Sequence 188, Appli

Sequence 189, Appli

Sequence 190, Appli

Sequence 191, Appli

Sequence 192, Appli

Sequence 193, Appli

Sequence 194, Appli

Sequence 195, Appli

RESULT 2
PCT-US92-06809-1

Sequence 1, Application PC/TU9206809

GENERAL INFORMATION:

APPLICANT: Ni, Jian
APPLICANT: Li, Haodong
APPLICANT: Yu, Guo-Liang
APPLICANT: Genitz, Reiner L
TITLE OF INVENTION: HUMAN CYSTATIN F

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/832,535
FILING DATE: 03-APP-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: KIMBALL, PAUL C.
REGISTRATION NUMBER: 34,610
REFERENCE/DOCKET NUMBER: PF265

TELECOMMUNICATION INFORMATION:

TELEPHONE: (201) 994-1700
TELEFAX: (201) 994-1744
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 145 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-832-535-2

Query Match Score 23.8%; DB 2; Length 145;
Best Local Similarity 31.6%; Pred. No. 9.4e-11;
Matches 37; Conservative 22; Mismatches 45; Indels 13; Gaps 3;

QY 11 TKICVGCRDPTNSPRLLELTHTKLNNENNATYFKIDNVKARVQVAGKRYFIDVFA 73
DB 32 SRYKPFFKTKTNDPVLQARYSYKEFNFCNTNDMFLKRSRITALVQIVKGKYMLE 91

QY 71 FVARETCSKESNEELITESCE--TKLGOSUDCNAAEVYYWPWEKIKIPTVNHWE 124
DB 92 VEIGTRCKKONHRL-DDCDPQTNHLKQTUSCYSEWVVPW-----LQHFE 138

RESULT 4
US-09-019-485-2

Sequence 2, Application US/09019485

GENERAL INFORMATION:

APPLICANT: Li, Haodong
APPLICANT: Yu, Guo-Liang
APPLICANT: Genitz, Reiner
APPLICANT: Ni, Jian
TITLE OF INVENTION: Cystatin F

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: US
ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

RESULT 3
US-08-832-535-2
Sequence 2, Application US/08832535
Patent No. 5919658

SOFTWARE: PatentIn Release #1.0, Version #1.3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/019,485
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Benson, Robert H.
 REGISTRATION NUMBER: 30,446
 REFERENCE/DOCKET NUMBER: PF265P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 3013098504
 TELEFAX: 3013098339
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 145 amino acids
 TYPE: amino acid
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 US-09-019-485-2

Query Match 23.8%; Score 163.5; DB 3; Length 145;
 Best Local Similarity 31.6%; Pred. No. 9.4e-11;
 Matches 37; Conservative 22; Mismatches 45; Indels 13; Gaps 3;
 Qy 11 TKICVGCPRDPTNSPEELTLLTIKLNAAENNATFYKIDNPKVQVAGKKYFID 70
 Db 32 SRVKPGPFKTIKNDPGVLAARSVEKFNCNTDMFLFKESSRITALVQVGLKMLE 91
 Qy 71 FVARETCSKESNEELTESC -- -TKKLGSQSLDCAEVYVPPKKIYPTVTNHWE 124
 Db 92 VEIGRTICKRNQHRL-DCCDFQTNTLKTQTLSCYSEWVVPW-----LQHFE 138

RESULT 5
 US-09-019-485-3
 Sequence 3, Application US/09019485
 Patent No. 6066617

GENERAL INFORMATION:
 APPLICANT: Li, Haodong
 APPLICANT: Yu, Guo-Liang
 APPLICANT: Gentz, Reiner
 APPLICANT: Ni, Jian
 TITLE OF INVENTION: Cystatin F
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: MD
 COUNTRY: US
 ZIP: 20850

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/019,485
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Benson, Robert H.
 REGISTRATION NUMBER: 30,446
 REFERENCE/DOCKET NUMBER: PF265P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 3013098504
 TELEFAX: 3013098339
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 145 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Linear

MOLECULE TYPE: protein
 US-09-019-485-3
 Query Match 23.8%; Score 163.5; DB 3; Length 145;
 Best Local Similarity 31.6%; Pred. No. 9.4e-11;
 Matches 37; Conservative 22; Mismatches 45; Indels 13; Gaps 3;
 Qy 11 TKICVGCPRDPTNSPEELTLLTIKLNAAENNATFYKIDNPKVQVAGKKYFID 70
 Db 32 SRVKPGPFKTIKNDPGVLAARSVEKFNCNTDMFLFKESSRITALVQVGLKMLE 91
 Qy 71 FVARETCSKESNEELTESC -- -TKKLGSQSLDCAEVYVPPKKIYPTVTNHWE 124
 Db 92 VEIGRTICKRNQHRL-DCCDFQTNTLKTQTLSCYSEWVVPW-----LQHFE 138

RESULT 6
 US-09-019-480-9
 Sequence 9, Application US/09431480
 Patent No. 6235708

GENERAL INFORMATION:
 APPLICANT: Holloway, James L.
 APPLICANT: Feldhaus, Andrew
 TITLE OF INVENTION: TESTIS SPECIFIC CYSTATIN-LIKE PROTEIN CYSTATIN T
 FILE REFERENCE: 98-72
 CURRENT APPLICATION NUMBER: US/09/431,480
 CURRENT FILING DATE: 1999-11-01
 EARLIER APPLICATION NUMBER: 60/109,217
 EARLIER FILING DATE: 1998-11-20
 EARLIER APPLICATION NUMBER: 60/156,382
 EARLIER FILING DATE: 1999-03-28
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 9
 LENGTH: 145
 TYPE: PPT
 ORGANISM: Homo sapiens
 US-09-019-480-9

Query Match 23.8%; Score 163.5; DB 3; Length 145;
 Best Local Similarity 31.6%; Pred. No. 9.4e-11;
 Matches 37; Conservative 22; Mismatches 45; Indels 13; Gaps 3;
 Qy 11 TKICVGCPRDPTNSPEELTLLTIKLNAAENNATFYKIDNPKVQVAGKKYFID 70
 Db 32 SRVKPGPFKTIKNDPGVLAARSVEKFNCNTDMFLFKESSRITALVQVGLKMLE 91
 Qy 71 FVARETCSKESNEELTESC -- -TKKLGSQSLDCAEVYVPPKKIYPTVTNHWE 124
 Db 92 VEIGRTICKRNQHRL-DCCDFQTNTLKTQTLSCYSEWVVPW-----LQHFE 138

RESULT 7
 US-09-617-302-9
 Sequence 9, Application US/09617302
 Patent No. 6245529

GENERAL INFORMATION:
 APPLICANT: Holloway, James L.
 APPLICANT: Feldhaus, Andrew
 TITLE OF INVENTION: TESTIS SPECIFIC CYSTATIN-LIKE PROTEIN CYSTATIN T
 FILE REFERENCE: 98-72 CL
 CURRENT APPLICATION NUMBER: US/09/617,302
 CURRENT FILING DATE: 2000-07-17
 PRIOR APPLICATION NUMBER: 09/431,480
 PRIOR FILING DATE: 1999-11-01
 PRIOR APPLICATION NUMBER: 60/109,217
 PRIOR FILING DATE: 1998-11-20
 PRIOR APPLICATION NUMBER: 60/156,382
 PRIOR FILING DATE: 1999-09-28
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 9
 LENGTH: 145

TYPE: PRT
ORGANISM: Homo sapiens
S-09-617-302-9

Query Match 23.8%; Score 163.5; DB 3; Length 145;
Best Local Similarity 31.6%; Pred. No. 9.e-11; Indels 13; Gaps 3;
Matches 37; Conservative 22; Mismatches 45; Application Data:
FILING DATE: Filed Herewith
CLASSIFICATION: 514
PRIORITY APPLICATION NUMBER: US/08/791,522
APPLICATION NUMBER: US/08/791,522
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0193 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: 30443
US-08-791-522-1

RESULT 8
S-09-528-436B-2
Sequence 2, Application US/09528436B
Patent No. 6576745
GENERAL INFORMATION:
APPLICANT: Li, et al.
TITLE OF INVENTION: Human Cystatin F
FILE REFERENCE: P2265P1D1
CURRENT APPLICATION NUMBER: US/09/528,436B
CURRENT FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 09/019,485
PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: 08/632,535
PRIOR FILING DATE: 1999-04-03
PRIOR APPLICATION NUMBER: 60/014,795
PRIOR FILING DATE: 1996-04-03
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 145
TYPE: PRT
ORGANISM: Homo sapiens
S-09-528-436B-2

Query Match 23.8%; Score 163.5; DB 4; Length 145;
Best Local Similarity 31.6%; Pred. No. 9.e-11; Indels 13; Gaps 3;
Matches 37; Conservative 22; Mismatches 45; Application Data:
FILING DATE: Filed Herewith
CLASSIFICATION: 514
PRIORITY APPLICATION NUMBER: US/09528436B
APPLICATION NUMBER: US/09528436B
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0193 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: 30443
US-08-791-522-1

Query Match 23.8%; Score 163.5; DB 2; Length 178;
Best Local Similarity 34.0%; Pred. No. 1.e-10;
Matches 35; Conservative 20; Mismatches 44; Indels 4; Gaps 2;
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Golik, Surya K.
TITLE OF INVENTION: NOVEL HUMAN CYSTATIN-LIKE
NUMBER OF SEQUENCES: 4
TITLE OF INVENTION: PROTEIN
CORESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ For Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/314,777
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION NUMBER: 08/791,522
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0193 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: 30443
US-08-791-522-1

RESULT 10
US-09-314-777-1
Sequence 1, Application US/09314777
Patent No. 611086
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Golik, Surya K.
TITLE OF INVENTION: NOVEL HUMAN CYSTATIN-LIKE
NUMBER OF SEQUENCES: 4
TITLE OF INVENTION: PROTEIN
CORESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ For Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/314,777
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION NUMBER: 08/791,522
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0193 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: 30443
US-08-791-522-1

RESULT 9
S-08-791-522-1
Sequence 1, Application US/08791522
Patent No. 5935517
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Golik, Surya K.
TITLE OF INVENTION: NOVEL HUMAN CYSTATIN-LIKE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ For Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/314,777
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION NUMBER: 08/791,522
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0193 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: 30443
US-08-791-522-1

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 178 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 CLONE: 30443

Query Match 23.7%; Score 163; DB 3; Length 178;
 Best Local Similarity 34.0%; Pred. No. 1.4e-10;
 Matches 35; Conservative 20; Mismatches 44; Indels 4; Gaps 2;

Qy 1 101 TKICIVGCPDRPTNSPEELTLTHITKLNAAENNATYFKIDNVKARVQVAGKKYFI 69
 Db 54 SRYKEPFPKTKTNDPGVQLARYSVEKFNFNCTNDMFLFESRITRALQIVKGKLMIE 113
 Qy 71 FVARETTCSKESNEELTESC--TKKLGOSLDCKNAEYVVPW 110
 Db 114 VEIGRTICKKQHRL-DDCFQTNTLKLQTLSCYSEWWVVPW 155

RESULT 13
 US-09-775-932-14

Sequence 14 Application US/09775932
 Patent No. 6534477

GENERAL INFORMATION:
 APPLICANT: University of British Columbia
 TITLE OF INVENTION: Production and use of Modified Cystatins
 FILE REFERENCE: 58069

CURRENT APPLICATION NUMBER: US/09/775,932
 CURRENT FILING DATE: 2001-02-02
 PRIOR FILING NUMBER: CA99/00717
 PRIOR FILING DATE: 1999-08-05
 PRIOR APPLICATION NUMBER: 60/095,503
 PRIOR FILING DATE: 1998-08-05
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 14
 LENGTH: 122
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-775-932-14

Query Match 20.2%; Score 138.5; DB 4; Length 121;
 Best Local Similarity 31.5%; Pred. No. 4.9e-08;
 Matches 34; Conservative 22; Mismatches 45; Indels 7; Gaps 3;

Qy 10 101 PTKICIVGCPDRPTNSPEELTLTHITKLNAAENNATYFKIDNVKARVQVAGKKYFI 69
 Db 2 2 QPERMTGELRDISPDPPQVRAQAQAVSNMGNSIYYFRDTHIKQASQLVAGKYFL 61

Query Match 20.2%; Score 138.5; DB 4; Length 128;
 Best Local Similarity 31.5%; Pred. No. 5.2e-08;
 Matches 34; Conservative 22; Mismatches 45; Indels 7; Gaps 3;

Qy 90 101 PTKICIVGCPDRPTNSPEELTLTHITKLNAAENNATYFKIDNVKARVQVAGKKYFI 69
 Db 69 TMEMGSTDCRKTRVTGDHVDLT-TCPLAGAQQEKLRCDFEVLPVPWQ 115

RESULT 13
 US-08-461-030C-2

Sequence 2 Application US/08461030C
 Patent No. 598361

GENERAL INFORMATION:
 APPLICANT: Ni, Jian
 APPLICANT: Yu, Guo-Liang
 APPLICANT: Gentz, Reiner
 APPLICANT: Rosen, Craig A.
 TITLE OF INVENTION: Human Cystatin E
 NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Ave
 CITY: Rockville
 STATE: MD
 COUNTRY: USA
 ZIP: 20850

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/461,030C
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: A. Anders, Brookes
 REGISTRATION NUMBER: 36,373
 REFERENCE DOCKET NUMBER: PF202
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 301-301-8504
 TELEFAX: 301-301-8339
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 149 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-461-030C-2

Query Match 20.2%; Score 138.5; DB 2; Length 149;
 Best Local Similarity 31.5%; Pred. No. 6.4e-08;
 Matches 34; Conservative 22; Mismatches 45; Indels 7; Gaps 3;

Qy 10 101 PTKICIVGCPDRPTNSPEELTLTHITKLNAAENNATYFKIDNVKARVQVAGKKYFI 69
 Db 30 QPERMTGELRDISPDPPQVRAQAQAVSNMGNSIYYFRDTHIKQASQLVAGKYFL 89

RESULT 12
 US-09-775-932-12

Sequence 12 Application US/09775932
 Patent No. 6534477

GENERAL INFORMATION:
 APPLICANT: University of British Columbia
 TITLE OF INVENTION: Production and use of Modified Cystatins
 FILE REFERENCE: 59069

CURRENT APPLICATION NUMBER: US/09/775,932
 CURRENT FILING DATE: 2001-02-02
 CURRENT FILING NUMBER: CA99/00717
 PRIOR APPLICATION NUMBER: CA99/00717
 PRIOR FILING DATE: 1998-08-05

RESULT 14
US-08-744-138-2
Sequence 2, Application US/08744138
Patent No. 6011012
GENERAL INFORMATION:
APPLICANT: Gentz, Reiner L.
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: Human Cystatin E
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPILER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/744,138
FILING DATE:
CLASSIFICATION: 425
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF202P1
TELEPHONE: 301 309 8504
TELEFAX: 301 309 8512
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-744-138-2

Query Match 20.2%; Score 138.5; DB 3; Length 149;
Best Local Similarity 31.5%; Pred. No. 6.4e-08;
Matches 34; Conservative 22; Mismatches 45; Indels 7; Gaps 3;
Ptkicvgcprdiptnspeleeltlthtklnaennnattyfkidnykkarvqavagkyfi 69
30 pqrmyvselrldspddpqvkaaoavasymngsnsiyyfrdthikaqolvagikyfl 89

Qy 10 Dfvarettcsks---sneeltesctkkgq-sldcnarevvypwe 111
Db 70 Dfvarettcske --- -sneeltesctkkgq -sldcnarevvypwe 111
Db 90 Tmemgstdcrktrvtgbhvdlt-tcpblaagaqqeklrcdfevlyvpwq 136

RESULT 15
US-09-431-480-8
Sequence 8, Application US/09431480
Patent No. 6235708
GENERAL INFORMATION:
APPLICANT: Holloway, James L.
APPLICANT: Feldhaus, Andrew
TITLE OF INVENTION: TESTIS SPECIFIC CYSTATIN-LIKE PROTEIN CYSTATIN T
FILE REFERENCE: 98-72
CURRENT APPLICATION NUMBER: US/09/431,480
EARLIER APPLICATION NUMBER: 60/109,217
EARLIER FILING DATE: 1998-11-20

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OM protein - protein search, using sw model

Run on: September 24, 2004, 14:05:18 ; Search time 36.576 Seconds
(without alignment)

1095.549 Million cell updates/sec

Title: US-10-661-784-3

Perfect score: 687

Sequence: 1 GSGKDFVQPPPTKICVGCPRD.....VPWEEKIYPTVTNNHWECEBF 127

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 31518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25:

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriopl:*
- 17: sp_archeap:*

SPTREMBL 25: *

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriopl:*

17: sp_archeap:*

ALIGNMENTS

RESULT 1

Q7YRP6 PRELIMINARY; PRT; 140 AA.

AC Q7YRP6; ID Q7YRP6; DT 01-OCT-2003 (TREMBLref, 25, Created)

DT 01-OCT-2003 (TREMBLref, 25, Last sequence update)

DT 01-OCT-2003 (TREMBLref, 25, Last annotation update)

DE Low molecular weight kininogen (Fragment).

GN Sus scrofa (Pig).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI TaxID=9823;

[1]

SEQUENCE FROM N.A.

RP Vonnahme K.A., Fernando S.C., Ross J.A., Ashworth M.D., Desilva U.,

RA Malayer J.R., Geisert R.D.,

RA "Pigine Endometrial and Conceptus Expression of Kininogens and Plasma

RT Kalikrein in Cyclic and Pregnant Gilts";

RT Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

RL DR EMBL; AY321363; AAP85260; 1; -.

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 140 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

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FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

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FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

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FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

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FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

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FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

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FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

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FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

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FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

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FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

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FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

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FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

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FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW; 177837836603F777 CRC64;

FT NON_TER 1 1 140 AA; 15650 MW;

RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 405:685-690(2000).
 DR EMBL; AB015224; BA34940.1; .
 DR EMBL; AK004420; BA323298.1; .
 DR HSSP; P01034; 1G96.
 DR MGI; MGI:1298217; Cst7.
 DR GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.
 DR InterPro; IPR00010; Cystatin.
 DR Pfam; PF00031; Cystatin; 1.
 DR SMART; SM0043; CY; 1.
 DR SEQUENCE 167 AA; 18847 MW; 61F76D8445095FE CRC64;
 SQ SEQUENCE 167 AA; 18847 MW; 61F76D8445095FE CRC64;

Query Match Score 22.2%; DB 13; Length 462;
 Best Local Similarity 38.8%; Pred. No. 8.4e-07;
 Matches 33; Conservative 13; Mismatches 34; Indels 5; Gaps 2;

Qy 4 KDFVQOPTKIVCGPPDIPNSPLEETLTITKLNAENNATYFKIDNVKARVQVAGK 63
 Db 50 KDLI---SSVKGPFPTTINNNPGVLAARKHSVEKFNNCTNDILFKBESHVSKALVQVTK 106

Qy 64 GKKYFIDFVARETTCSKESNEELTESC--TKKLGSQSLDCNAEVYVVW 110
 Db 107 GLKYMLEVKGRTTCRKTMEHQL-DNCDFTQTNPAKRTLYCYSEWWVIIW 155

RESULT 5
 Q7ZAJ8 PRELIMINARY; PRT; 167 AA.
 ID Q7ZAJ8 PRELIMINARY;
 AC DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Cystatin F (Leukocystatin).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1] _
 RP SEQUENCE FROM N.A.

Kalnine N., Chen X., Rollis A., Halleck A., Hines L., Eisenstein S.,
 RA Koundinya M., Raphael J.U., Moreira D., Kelley T., LaBaer J., Lin Y.,
 RA Phelan M., Farmer A.;
 RA Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BT009825; AAP8827.1; .
 DR EMBL; BT009825; AAP8827.1; .
 SQ SEQUENCE 167 AA; 18857 MW; E3339025A5BD60177 CRC64;

Query Match Score 23.0%; DB 4; Length 167;
 Best Local Similarity 31.6%; Pred. No. 2.1e-08;
 Matches 37; Conservative 22; Mismatches 45; Indels 13; Gaps 3;

Qy 11 TKICVGCGPDRDIPNSPLEETLTITKLNAENNATYFKIDNVKARVQVAGKFLD 70
 Db 54 SRVKPGPPTKIKNDPVLQARYSTKEFKNFNTDMFLKESRITRALLQVKGKYM 113

Qy 71 FYARETTCSKESNEELTESC--TKKLGSQSLDCNAEVYVVWEEKIYPVTVNHW 124
 Db 114 VEIGRTICKKQNOHLRL-DDCDFQTNTHLQKOTLSCYSEWWVTPW-----LOHFE 160

RESULT 6
 Q7ZY91 PRELIMINARY; PRT; 462 AA.
 ID Q7ZY91 PRELIMINARY;
 AC DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Similar to fetuin B.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC NCBI_TaxID=8355;

RN [1] _
 RP SEQUENCE FROM N.A.

Costa R.M.B., Mason J., Lee M., Amaya E., Zorn A.M.;
 RA "Novel gene expression domains reveal early patterning of the Xenopus
 endoderm";
 RA Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AY260732; AAP88289.1; .
 DR EMBL; AY260732; AAP88289.1; .
 SQ SEQUENCE 462 AA; 53186 MW; 796F92774CC2721 CRC64;

Query Match Score 22.2%; DB 13; Length 462;
 Best Local Similarity 38.8%; Pred. No. 8.4e-07;
 Matches 33; Conservative 13; Mismatches 34; Indels 5; Gaps 2;

Qy 10 PTKICVGCGPDRDIPNSPLEETLTITKLNAENNATYFKIDNVKARVQVAGK 65
 Db 142 PGVLISTCP-DCPTANEEPTPTTADTLIAEYNKDSNNTRYFKIDHIERVRSQWVGP 200

Qy 66 KYFDIDFVARETTCSKESNEELTESC 90
 Db 201 SYFQFTKETDKMKTOENVVLNSNC 225

RESULT 8
 Q801E5 PRELIMINARY; PRT; 465 AA.
 ID Q801E5 PRELIMINARY;
 AC DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical histidine-rich protein (Fragment).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC NCBI_TaxID=8355;

OX	NCBI_TaxID=8355;	Qy	75 ETTCCSKSNEELTESC---ETTKLUGQSILDCNAEYYYYPWEKKIYPTVTVNHWCE 126
RN	SEQUENCE FROM N.A.; PubMed=12591597;	Db	90 RITCTK-SQTNLTD-CSPHDQPHMRALCSQIYSSPVWKK---GTHSLTNFSCK 138
RX	Medline=2280013; PubMed=12591597;		
RA	Chen Y., Jurgens K., Hollmann T., Claussen M., Ramadori G.,		
RA	Pielier T.;		
RT	"Cell-autonomous and signal-dependent expression of liver and	RESULT 10	
RT	intestine marker genes in pluripotent precursor cells from Xenopus embryos.,"	Q800SB	
RT	Mech. Dev. 120:277-288 (2003).	ID	PRELIMINARY;
RL	EMBL: AY18284; AAC31610_1.;	AC	PRT; 455 AA.
DR	GO: GO:000869; F: cysteine protease inhibitor activity; IEA.	DT	Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR	InterPro: IPR000010; Cystatin.	DT	01-JUN-2003 (TRINBLrel. 24, Last sequence update)
DR	Pfam: PF00031; Cystatin; 2.	DT	01-OCT-2003 (TRINBLrel. 25, Last annotation update)
DR	SMART; SM00043; CY_2.	DB	Fetuin-A.
FT	Hypothetical protein.	OS	Brachydanio rerio (zebrafish) (Danio rerio).
FT	NON_TER 1	OC	Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
SQ	SEQUENCE 465 AA; 53528 MW; 0B403AB4578BBFD4 CRC64;	OC	NCBI_TaxID=7955;
		OX	
		RN	
		RP	SEQUENCE FROM N.A.
		RC	Jia F.,
		TISSUE=Liver;	RT
			"Danio rerio fetuin-A,"
			RL
			Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
			DR
			EMBL: AX17558; AA061483_1.;
			GO; GO:000584; C: microtubule; IEA.
			DR
			GO; GO:0004869; F: cysteine protease inhibitor activity; IEA.
			DR
			GO; GO:0005198; F: structural molecule activity; IEA.
			DR
			InterPro: IPR02453; Beta tubulin.
			DR
			InterPro: IPR000010; Cystatin.
			DR
			PFam; PF00031; cystatin; 1.
			DR
			SMART; SM00043; CY_1.
			DR
			PROSITE; PS00228; TUPULIN_B_AUTOREG_1.
			SQ
			SEQUENCE 455 AA; 50627 MW; D822872926BA2ACB CRC64;
Qy	10 PTIKICGCPDITPTNSPELEETLTHTI---ITKLNAENNAATFYFKIDNVKKARYQVVAKG 65	Query Match	18.0% Score 123.5;
Best Local Similarity	38.8%; Pred. No. 8.5e-07;	Best Local Similarity	26.7% Pred. No. 0.00053;
Matches	33; Conservative 13; Mismatches 34; Indels 5; Gaps 2;	Matches	23; Mismatches 46; Indels 19; Gaps 4;
Db	145 PEVILSTCP-DCTPTEITPTTAETLIAEYNDTSNNTRYFKIDHTERVSRQWVCP 203	DR	Score 123.5;
Qy	66 KYFIDFVARTEITCSKESNEELTESC 90	Qy	2 SGKDFVQOPTKICVGCPDRDPTNSPELEETLTHTITKLNAENNAATFYFKIDNVKKARYQ-
Db	204 SYFOFTKETDCMKTQENVVLSNC 228	Db	60 DR
			SHEDLV---KRCPDCHGLPLHEPKALESYNAALAKFNQSNHKSYFKEVGRISQSW 189
			DR
			61 VHAGKRFIDFVARETCSKESNEELTESC-----CERKLIG-QSLDNAEVY 106
			DR
			190 MPNGQSTFTQFAIMETNCTKDAPONPEACKALCGDQATYFCRKSXVGSEEPVECEVY 249
			DR
RESULT 9		DR	
Q9BPX9	Q9EPX9 PRELIMINARY; PRT; 140 AA.	Q8CB17	PRELIMINARY;
ID	AC Q9EPX9_	ID	PRT; 388 AA.
AC	Q9EPX9_	AC	
DT	01-MAR-2001 (TRINBLrel. 16, Created)	DT	
DT	01-MAR-2001 (TRINBLrel. 16, Last sequence update)	DT	
DT	01-MAR-2003 (TRINBLrel. 24, Last annotation update)	DT	
DE	Cystatin_C.	DT	
OS	Mus musculus (Mouse).	DT	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	DT	
OC		DE	
NCBI_TaxID=10090;		DE	
RN	SEQUENCE FROM N.A.	DE	
RP		DE	
RC	STRAIN=BALB/C;	DE	
RX	Medline=21010502; PubMed=11144350;	GN	
RA	Taupin P.J., Ray J., Fischer W.H., Suhre S.T., Hakansson K., Grubb A.,	OS	
RA	Gage F.H.	OS	
RA	"EGF-2-Responsive neural stem cell proliferation requires CCG, a novel autocrine/paracrine cofactor."	OC	
RT	RT	OC	
RT	Neuron 28:385-397 (2000).	NCBI_TaxID=10090;	
RL	DR	RN	
DR	HSSP; P01034; IG96.	RC	
DR	GO; GO:000869; F: cysteine protease inhibitor activity; IEA.	RC	
DR	InterPro: IPR000010; Cystatin.	RC	
DR	Pfam; PF00031; Cystatin; 1.	RC	
DR	SMART; SM00043; CY_1.	RC	
DR	PROSITE; PS00287; CYSTATIN; 1.	RC	
FT	CHAIN 21 140 CYSTATIN C.	RC	
FT	VARIANT 16 84 A -> G.	RC	
FT	VARIANT 84 84 L -> F.	RC	
SQ	SEQUENCE 140 AA; 15517 MW; 3A53405DD58D785 CRC64;	RC	
		SEQUENCE FROM N.A.	
		STRAIN=C57BL/6J; TISSUE=Vagina;	
		MEDLINE=2235468; PubMed=1246651;	
Query Match	19.1%; Score 131.5; DB 11;	RX	
Best Local Similarity	27.8%; Pred. No. 2.6e-05;	RA	The FANTOM Consortium,
Matches	32; Conservative 26; Mismatches 48; Indels 9; Gaps 4;	RA	the RIKEN Genome Exploration Research Group Phase I & II Team;
Qy	15 VGCPDRDPTNSPELEETLTHTITKLNAENNAATFYFKIDNVKKARYQVAGKCFIDFVAR 74	RT	"Analysis of the mouse transcriptome based on functional annotation of
Db	30 LGAPEEADANESEGVRRALDFAVSEINKGSNDAYHSRAIQVVRARKQLVAGVNFLDVMG 89	RT	60,770 full-length cDNAs."
		RL	Nature 420:563-573 (2002);
		DR	EMBL; AK037043; BAC9682.1.;
		DR	MGD; MGI:1890222; Fetub.

DR GO; GO:0004869; Picysteine protease inhibitor activity; IEA.

DR InterPro; IPR00010; Cystatin.

DR InterPro; IPR00013; Cystatin.

DR Pfam; PF00031; Cystatin.

DR SMART; SM00043; CYT.

DR PROSITE; PS01254; FETUIN 1; 1.

DR PROSITE; PS01255; FETUIN 2; 1.

DR PROSITE; PS01256; FETUIN 2; 1.

DR SEQUENCE; 388 AA; 42/42 MW;

SQ 78CPADD7A8D9DC22 CRC64;

Query Match 17.3%; Score 119; DB 11; Length 38;

Best Local Similarity 25.9%; Pred. No. 0.015%; Indels 6; Gaps 3;

Matches 30; Conservative 28; Mismatches 52; RT "Characterization and immunological properties of a cystein protease

RT inhibitor of the filarial parasite Litomosoides sigmodontis.";

RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF224173; AAP55961; -.

DR GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.

DR InterPro; IPR000010; Cystatin.

DR Pfam; PF00031; Cystatin.

DR SMART; SM00043; CYT.

DR PROSITE; PS00287; CYSTATIN; 1.

DR CHAIN 25 148 LS-CYSTATIN.

SQ 295CAA89CA5329C9 CRC64;

RESULT 12

DR Q80125 PRELIMINARY; PRT; 464 AA.

AC Q80125; ID Q80125; PRELIMINARY; PRT; 464 AA.

DR 01-JUN-2003 (TREMBLref. 24, Created)

DR 01-OCT-2003 (TREMBLref. 24, Last sequence update)

DR 01-OCT-2003 (TREMBLref. 25, Last annotation update)

DE Petuin long form.

OS Cyprinus carpio (Common carp).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

Cyprinidae; Cyprinidae; Cyprinidae.

OX NCBI TaxID=7962;

RN [1]

RP SEQUENCE FROM N.A.

RA Tsai P.-L.; Chang G.-D.; Huang C.-J.;

RT "Purification and cloning of carp fetuin."

RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY225965; AAC04862; 1.

DR GO; GO:0005874; C:microtubule; IEA.

DR GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR GO; GO:0007018; P:microtubule-based movement; IBA.

DR InterPro; IPR002453; Beta-tubulin.

DR InterPro; IPR00010; Cystatin.

DR Pfam; PF0031; Cystatin; 1.

DR PROSITE; PS00228; TUBULIN_B_AUTOREG; 1.

DR SMART; SM00043; CYT.

DR SEQUENCE; PS00228; TUBULIN_B_AUTOREG; 1.

SQ 51698 MW; 7A54F7E44050895 CRC64;

Query Match 17.1%; Score 117.5; DB 13; Length 464;

Best Local Similarity 24.8%; Pred. No. 0.0025%; Indels 15; Gaps 4;

Matches 32; Conservative 23; Mismatches 59; RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16809-16903 (2002).

RN [2]

RESULT 13

DR Q9NH95 PRELIMINARY; PRT; 148 AA.

AC Q9NH95; ID Q9NH95; PRELIMINARY; PRT; 148 AA.

BLOSUM62						
Scoring table: BLOSUM62						
Sequence: 1 GSSKDFVQPPTRKICVGCPRD.....VPMEEKKIYPTVTVNHNCEFP 127						
Search results:						141681 seqs., 52070155 residues
Total number of hits satisfying chosen parameters:						141681
Minimum DB seq length: 0						
Maximum DB seq length: 2000000000						
Post-processing: Minimum Match 0%						Maximum Match 100%
Listing first 45 summaries						SwissProt_42::*
Database : GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.						
Run on: September 24, 2004, 14:04:32 ; Search time 8.636 Seconds (without alignments) 765.738 Million cell updates/sec						
Title: US-10-661-784-3						
Perfect score: 687						
Sequence: CYTA-SARPE Q9d269 mus musculu Q9h114 homo sapien P322765 mus musculu P296592 mus musculu O606756 homo sapien P81714 rata atra (Homo sapien) Q9h112 homo sapien P28325 homo sapien P31726 zea mays (Maize) P24090 rattus norvegicus (Rat) P02765 homo sapien						
Alignments						
RESULT 1						
KNG_HUMAN	STANDARD;	PRT;	644 AA.			
ID	KNG_HUMAN	STANDARD;	PRT;			
AC	P01042; P01043;	PRINTER;	01, Created)			
DT	21-JUL-1985 (Rel. 01,	SEQUENCE FROM N.A. (ISOFORMS HMW AND LMW).				
DT	01-FEB-1995 (Rel. 33,					
DT	Last sequence update					
DB	10-OCT-2003 (Rel. 42,					
DB	Last annotation update					
DE	Kininogen Precursor (Alpha-2-thiol proteinase inhibitor)	[Contains:				
GN	Bradykinin].					
KG	Homo sapiens (Human).					
OS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A. (ISOFORMS HMW AND LMW).					
RC	TISSUE=Liver;					
RX	MDLINE=85234532; PubMed=2989293;					
RA	Takagaki Y., Kitamura N., Nakashita S.; Cloning and sequence analysis of cDNAs for human high molecular weight prekininogens. Primary structures of two human prekininogens. J. Biol. Chem. 260:8601-8609(1985).					
RN	[2]					
RP	GENE STRUCTURE. MEDLINE=85234533; PubMed=2989294;					
RX	Kitamura N., Kitagawa H., Fukushima D., Takagaki Y., Miyata T., Nakashita S.; Isolation of a human cDNA for alpha-2-hydroxy proteinase inhibitor and its evolution. J. Biol. Chem. 260:8610-8617(1985).					
RN	[3]					
RP	SEQUENCE OF 1-401 FROM N.A. MEDLINE=8512622; PubMed=4054110;					
RX	Okubo I., Kuruchi K., Takasawa T., Shiokawa H., Sasaki M.; Isolation of a human cDNA for alpha-2-hydroxy proteinase inhibitor and its identity with low molecular weight kininogen. J. Biochemistry 23:15691-5697(1984).					
RN	[4]					
RP	SEQUENCE OF 379-644. MEDLINE=86030270; PubMed=4054110;					
RX	Lottspeich F., Kelleermann J., Henschchen A., Foertsch B., Mueller-Berger W.; The amino acid sequence of the light chain of human high-molecular-mass kininogen. R. J. Biochem. 152:307-314(1985).					
RN	[5]					
RP	SEQUENCE OF 381-389. MEDLINE=90355622; PubMed=4952632;					
RX	Pierce J.V.; Structural features of plasma kinins and kininogens. R. J. Biochem. 152:307-314(1985).					
RA	Ped. Proc. 27:52-57(1988).					
RN	[6]					
RP	Sueyoshi T., Miyata T., Kato H., Iwanaga S.; Disulfide bonds in bovine HMW kininogens. R. J. Biochem. 152:307-314(1985).					
PA	"Disulfide bonds in bovine HMW kininogens." R. J. Biochem. 152:307-314(1985).					
RT	R. J. Biochem. 152:307-314(1985).					

Seikagaku 56:808-808 (1984).

[7] CARBOHYDRATE-LINKAGE SITE ASN-294.

RN MEDLINE-22660472; PubMed=12754519.

RX Zhang H.; Li X.-J.; Martin D.B.; Abersold R.;

RA Identicality and quantification of N-linked glycoproteins using

RT hydrazide chemistry, stable isotope labeling and mass spectrometry. ";

RL Nat. Biotechnol. 21:660-666(2003).

CC -1- FUNCTION: (1) Kininogen is inhibitors of thiol proteases; (2)

CC HMW kininogen plays an important role in blood coagulation by

CC helping to position optimally prekallikrein and factor XI next to

CC factor XII; (3) HMW-kininogen inhibits the thrombin-and plasmin-

CC induced aggregation of thrombocytes; (4) the active peptide

CC bradykinin that is released from HMW-kininogen shows a variety of

CC physiological effects: (4A) inflation in smooth muscle

CC contraction, (4B) induction of hypotension, (4C) natriuresis and

CC diuresis, (4D) decrease in blood glucose level, (4E) it is a

CC mediator of inflammation and causes (4E1) increase in vascular

CC permeability, (4E2) stimulation of nociceptors (4E3), release of

CC other mediators of inflammation (e.g. prostaglandins), (4F) it has

CC a cardioprotective effect (directly via bradykinin action); (5)

CC indirectly via endothelium-derived relaxing factor action; (6)

CC HMW-kininogen inhibits the aggregation of thrombocytes; (6)

CC kininogen is in contrast to HMW-kininogen not involved in blood

CC clotting.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=HMW;

CC IsoID=P01042-1; Sequence-Displayed;

CC Name=LmW;

CC IsoID=P01042-2; Sequence=VSP_001261, VSP_001262;

CC -1- TISSUE SPECIFICITY: Plasma.

CC -1- PTM: Bradykinin is released from plasma kallikrein.

CC -1- SIMILARITY: Contains 3 cystatin-like domains.

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CC -----

DR EMBL; K02566; AAA35497.1;

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DR EMBL; M11699; AAB59550.1;

DR EMBL; M11700; AAB59550.1;

DR EMBL; M11701; AAB59550

21-JUL-1986 (Rel. 01, Last sequence update)
 DT LMW-2040 (Rel. 43, Last annotation update)
 DE Kininogen, LMW I precursor (Thiol protease inhibitor) [Contains:
 Bdrykinin].
 DE Bovine.
 OS Bos taurus; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1] _
 RN SEQUENCE FROM N.A.
 RX MEDLINE=33117059; PubMed=6572010;
 RA Nawa H., Kitamura N., Hirose T., Asai M., Inayama S., Nakaniishi S.;
 RT "Primary structures of bovine liver low molecular weight kininogen
 precursors and their two mRNAs.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:90-94 (1983).
 RN [2]
 RP SEQUENCE OF 19-378.
 RX MEDLINE=81137330; PubMed=3546295;
 RA Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H.,
 Miyata T., Iwanaga S.;
 RT "Bovine high molecular weight kininogen. The amino acid sequence,
 positions of carbohydrate chains and disulfide bridges in the heavy
 chain portion.";
 RL J. Biol. Chem. 262:2768-2779 (1987).
 CC -!- FUNCTION: (1) Kininogens are inhibitors of thiol proteases; (2)
 CC LMW-kininogen inhibits the aggregation of thrombocytes; (3) the
 active peptide kallidin that is released from LMW-kininogen shows
 a variety of physiological effects: (3A) influence in smooth
 muscle contraction, (3B) induction of hypertension, (3C)
 CC nature and diuresis (kidney).
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- ALTERNATIVE PRODUCTS:
 Event-Alternative splicing; Named isoforms=2;
 CC Name=LMW I;
 CC IsoId=P01046-1; Sequence=Displayed;
 CC Name=LMW I;
 CC IsoId=P01044-1; Sequence=External;
 CC -!- TISSUE SPECIFICITY: Plasma.
 CC -!- PTM: Bradykinin is released from kininogen by plasma kallikrein.
 CC -!- MISCELLANEOUS: LMW-kininogen is in contrast to HMW-kininogen not
 CC involved in blood clotting.
 CC -!- SIMILARITY: Contains 3 cystatin-like domains.
 CC --- This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 DR EMBL; V00426; CAA23709.1; -.
 DR InterPro: IPR00010; Cystatin.
 DR Pfam; PF00031; Cystatin_3.
 DR SMART; SM0043; CY_3.
 DR PROSITE; PS00287; CYSTATIN_2.
 KW Glycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing;
 KW Thiol protease inhibitor; Bradykinin; Signal;
 KW Pyrrolidone carboxylic acid.
 FT SIGNAL 1 18
 FT DOMAIN 136 257
 FT CHAIN 19 436
 FT PEPTIDE 19 378
 FT CHAIN 380 388
 FT DOMAIN 389 436
 FT DOMAIN 19 135
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 FT CARBOHYD 87 87
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 FT CARBOHYD 168 168
 FT CARBOHYD 197 197
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 FT DISULFID 295 295
 FT CONFLICT 436 AA; 48427 MW; F01FTEB6614BEGC CRC64;
 SQ SEQUENCE 436 AA; Score 440%; Score 440%; DB 1; Length 436;
 Query Match 64.0%; Best Local Similarity 70.4%; Matches 14; Pred. No. 1; DB 1; Gaps 0; Gaps 0;
 Matches 81; Conservative 20; Indels 0; Gaps 0;
 QY 4 KDFVQOPTKICVGCPDPIDPINSPELETLIGHTITKINDENNATEYKIDNYKKARVQVA 63
 DB 253 KDFVQOPTKICVGCPDPIDPINSPELETLIGHTITKINDENNATEYKIDNYKKARVQVA 312
 QY 64 GKRYFDEVARETTCSKESNEBLTESETKLGSQSLDCAEAYVVEWEKKIPTY 118
 DB 313 GKYSIVTIVIARETTCSKESNEBLTESETKLGSQSLDCAEAYVVEWEKKIPTY 367
 RESULT 3
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 ID_KNNI_BOVIN STANDARD; PRT; 621 AA.
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 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Kininogen, HMW I precursor (Thiol protease inhibitor) [Contains:
 DE Bradykinin].
 DE Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84014106; PubMed=6571699;
 RA Kitamura N., Takegaki Y., Furuto S., Tanaka T., Nawa H., Nakaniishi S.;
 RA "A single gene for bovine high molecular weight and low molecular
 weight kininogens.";
 RA Nature 305:545-549 (1983).
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 RA Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H.,
 RA "Studies on the structure of bovine kininogen: cleavages of disulfide
 bonds and of methionyl bonds in kininogen-II.";
 RA J. Biol. Chem. 262:2768-2779 (1987).
 [3]
 RN SEQUENCE OF 378-393.
 RX MEDLINE=70180420; PubMed=4986212;
 RA Kato H., Nagasawa S., Suzuki T.;
 RA "Bovine high molecular weight kininogen. The amino acid sequence,
 RT positions of carbohydrate chains and disulfide bridges in the heavy
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 RT J. Biol. Chem. 262:2768-2779 (1987).
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 RN SEQUENCE OF 458-498.
 RX MEDLINE=75170265; PubMed=1169237;
 RA Han Y.N., Konishi M., Iwanaga S., Suzuki T.;
 RA "Studies on the primary structure of bovine high-molecular-weight
 kininogen. Amino acid sequence of a fragment ("histidine-rich
 peptide") released by plasma kallikrein.";
 RT J. Biochem. 67:313-323 (1970).
 RL CC -!- FUNCTION: (1) Kininogens are inhibitors of thiol proteases;

HMW-kininogen plays an important role in blood coagulation by helping to position optimally prekallikrein and factor XI next to factor XII; (3) HMW-kininogen inhibits the thrombin- and plasmin-induced aggregation of thrombocytes; (4) the active peptide bradykinin that is released from HMW-kininogen shows a variety of physiological effects: (4A) influence in smooth muscle contraction, (4B) induction of hypotension, (4C) natriuresis and diuretics, (4D) decrease in blood glucose level, (4E) it is a mediator of inflammation and causes (4E1) increase in vascular permeability, (4E2) stimulation of nociceptors (4E3) release of other mediators of inflammation (e.g. prostaglandins), (4F) it has a cardioprotective effect (directly via bradykinin action), (4G) it has indirectly via endothelium derived relaxing factor action).

- !- SUBCELLULAR LOCATION: Extracellular.
- !- ALTERNATIVE PRODUCTS:
- !- Event:Alternative splicing; Named isoforms=2;
- !- Name=HMW I;
- !- IsoId=P01044-1; Sequence=Displayed;
- !- Name=HMW I;
- !- IsoId=P01046-1; Sequence=External;
- !- TISSUE SPECIFICITY: Plasma.
- !- PTM: Bradykinin is released from kininogen by plasma kallikrein.
- !- SIMILARITY: Contains 3 cystatin-like domains.

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EMBL; V01491; CAA24735.1;	-	
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InterPro; IPR000110; Cystatin.		
InterPro; IPR002395; Kininogen.		
PRINTS; PRO0334; KININGEN.		
SMART; SM00434; CY, 3.		
PSI-PROTEIN; PS00287; CYSTATIN; 2.		
Glycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing;		
Thiol_protease_inhibitor; Bradykinin; Blood coagulation;		
Inflammatory response; Signal; Pyroline carboxylic acid.		
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CHAIN	389	LIGHT CHAIN.
DOMAIN	1.9	CYSTATIN-LIKE 1.
DOMAIN	1.36	CYSTATIN-LIKE 2.
DOMAIN	258	CYSTATIN-LIKE 3.
MOD_RES	1.9	PYRROLIDONE CARBOXYLIC ACID.
CARBODY	87	N-LINKED (GLCNAC. . .).
CARBODY	136	O-LINKED (PARTIAL). . .
CARBODY	168	N-LINKED (GLCNAC. . .) (OR 169).
CARBODY	197	N-LINKED (GLCNAC. . .) (PARTIAL).
CARBODY	204	N-LINKED (GLCNAC. . .).
DISULFID	27	INTERCHAIN.
DISULFID	591	
DISULFID	82	
DISULFID	93	
DISULFID	106	
DISULFID	125	
DISULFID	141	
DISULFID	144	
DISULFID	205	
DISULFID	217	
DISULFID	228	
DISULFID	247	
DISULFID	263	
DISULFID	327	
DISULFID	339	
DISULFID	350	
SORTING	369	
DISULFIDE	636	
DISULFIDE	650	
DISULFIDE	651	
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DISULFIDE	997	
DISULFIDE	998	
DISULFIDE	999	
DISULFIDE	1000	

Query Match 64.0%; Score 440; DB 1; Length 621;
 Best Local Similarity 70.4%; Pred. NO. 2.76-34;
 Matches 81; Conservative 14; Mismatches 20; Indels 0; Gaps 4

DR HSSP; P01038; 1A90.
 DR InterPro; IPR00010; Cystatin.
 DR Pfam; PF00031; cystatin; 3.
 DR SMART; SM00043; CY; 3.
 DR PROSITE; PS00087; CYSTATTIN; 2..

KW	Thiol protease inhibitor; Bradykinin; Signal;
KW	Pyroglutidone carboxylic acid.
FT	18 KININOGEN, LMW II.
CHAIN	19 434 HEAVY CHAIN.
CHAIN	19 376 LIGHT CHAIN.
PEPTIDE	378 386 BRADYKININ.
FT	387 434 CYSTATIN-LIKE 1.
CHAIN	19 135 CYSTATIN-LIKE 2.
DOMAIN	136 256 CYSTATIN-LIKE 3.
DOMAIN	257 376 PYRROLIDONE CARBOXYLIC ACID.
MOD RES	19 19 N-LINKED (GLCNAC. .).
CARBOHYD	87 87 O-LINKED (PARTIAL. .).
FT	CARBOHYD 136 136 (OR 169).
CARBOHYD	168 168 N-LINKED (GLCNAC. .) (PARTIAL).
FT	CARBOHYD 197 197 N-LINKED (GLCNAC. .) (PARTIAL).
CARBOHYD	204 204 N-LINKED (GLCNAC. .).
CARBOHYD	280 280 N-LINKED (GLCNAC. .).
FT	INTERCHAIN.
DISULFID	27 404
FT	DISULFID 82 93
DISULFID	106 125
FT	DISULFID 141 144
DISULFID	205 217
FT	DISULFID 228 247
DISULFID	261 264
FT	DISULFID 325 337
DISULFID	348 367
SEQUENCE	434 AA; 48148 MW; 73A7079DBE30430 CRC64;
Query	Query Match 60.1%; Score 413; DB 1; Length 434;
Matches	Best Local Similarity 67.2%; Pred. No. 6.6e-22; Index 2; Gaps 1;
88	Mismatches 14; Mismatches 14; Standard; PRT; 619 AA.
Qy	3 GKDFVQQPTKICVGCPDRDIPNTNSPELETHTHTKLNAAENNATTFPKIDVNKKKARQVV 62
Db	252 GDEFEL-PPMVYCVGCFKPPIPVDSPDIEALNHSSIAEHDGTFFKIDVYKVKATVQVV 309
Qy	63 AGKXKFIDFARETTTSKESNEELTSCETTRKLQGQLDCNAEVYYVPPWERKLYPTV 118
Db	310 GGLKXSYIVPIARETICSKGNSNEELTKSCEINHGQILHCDANVYVPPWERKLYPTV 365
RESULT 5	
ID	KNH_BOVIN STANDARD; PRT; 619 AA.
KNH2_BOVIN	SEQUENCE FROM N.A.
ID	KNH2_BOVIN PRT; 619 AA.
AC	P01045; MEDLINE=8001416; PubMed=6571699;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Kininogen, LMW II Precursor (thiol proteinase inhibitor) (Contains:
DE	Bradykinin).
OS	Bos taurus (Bovine).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Butharia; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC	Bovidae; Bovine; Bos.
OX	NCBI_TaxID=9913;
RN	[1] SEQUENCE FROM N.A.
RX	MEDLINE=80137530; PubMed=3546295;
RX	Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H.,
RA	Kitamura N., Takagaki Y., Furuto S., Tanaka T., Nawa H., Nakanishi S.;
RA	"A single gene for bovine high molecular weight kininogen. The amino acid sequence, RT positions of carbohydrate chains and disulfide bridges in the heavy chain portion." RT
RT	J. Biol. Chem. 262:2768-2779 (1987). RT
RL	[2] SEQUENCE OF 19-376.
RN	RP MEDLINE=80137530; PubMed=3546295;
RX	Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H.,
RA	Miyata T., Iwaga S.,
RA	"Bovine high molecular weight kininogen. The amino acid sequence, RT positions of carbohydrate chains and disulfide bridges in the heavy chain portion." RT
RT	J. Biol. Chem. 262:2768-2779 (1987). RT
RL	[3] SEQUENCE OF 376-391.
RN	RP

- FT DOMAIN 257 376 CYSTATIN-LIKE 3, PYRROLIDONE CARBOXYLIC ACID.
- FT MOD RES 19 19 RA Nagashima T., Numata K., Okido T., Pavan W.J., Perrea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ringerwald M., Ravasi T., Reid J.C., Reid D.J., Reid J., Riing B.Z., Rigwawald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Tessdale R.D., Tonita M., Verardo R., Wagner L., Wanlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yang S.I., Yang T., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishizaki T., Konno H., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imamura K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation of RT RT full-length cDNAs"; Nature 420:563-573(2002). [3]
- FT DISULFID 125 RN RP SEQUENCE FROM N.A. (ISOFORM LMW).
- FT DISULFID 144 RA TISSUE-liver; MEDLINE=22388257; PubMed=12477932;
- FT DISULFID 205 RA strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Scheuer C.F., Bhat N.K., Alischul S.F., Zeberg B., Buetow K.H., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stepleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalona D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Falley J., Heitton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E., Scherzer A., Schein J.E., Jones S.J.M., Marza M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
- FT DISULFID 228 RA -!- FUNCTION: (1) Kininogen are inhibitors of thiol proteases; (2) HMW-kininogen plays an important role in blood coagulation by helping to position optimally prekallikrein and factor XI next to factor XII; (3) HMW-kininogen inhibits the thrombin-and plasmin-induced aggregation of thrombocytes; (4) the active peptide bradykinin that is released from HMW-kininogen shows a variety of physiological effects (4A) influence in smooth muscle contraction, (4B) induction of hypotension, (4C) natriuresis and diuresis, (4D) decrease in blood glucose level, (4E) it is a mediator of inflammation and causes (4E1) increase in vascular permeability, (4E2) stimulation of nociceptors (4E3) release of other mediators of inflammation (e.g. prostaglandins); (4F) it has a cardioprotective effect (directly via bradykinin action); (5) indirectly via endothelium-derived relaxing factor action; (5) HMW-kininogen inhibits the aggregation of thrombocytes; (6) HMW-kininogen is in contrast to HMW-kininogen not involved in blood clotting (By similarity).
- FT DISULFID 261 RA -!- SUBCELLULAR LOCATION: Secreted.
- FT DISULFID 264 RA -!- ALTERNATIVE PRODUCTS:
- FT VARIANT 325 RX Event=Alternative splicing; Named isoforms;
- FT VARIANT 337 RN Name=HMW;
- FT VARIANT 367 RA IsoID=008677-1; Sequence=Displayed;
- FT VARIANT 398 RA Name=LMW;
- FT VARIANT 401 RA IsoID=008677-2; Sequence=VSP_001264;
- FT VARIANT 454 RA -!- TISSUE SPECIFICITY: Plasma.
- SQ SEQUENCE 619 AA; 68710 MW; F043.0A8BE00E0DA CRC64; CC -!- PTM: Bradykinin is released from kininogen by Plasma kallikrein.
- Query March 60.1% Score 413; DB 1; Length 619; Best Local Similarity 67.2%; Pred. No. 9.9e-32; Matches 78; Conservative 14; Mismatches 22; Indels 2; Gaps 1;
- Qy 3 GKDVFQPPTKICPGCPDIPTNSPELEITLTITKLNAAENNATPFKIDNPKKARYQV 62 RA -!- SIMILARITY: Contains 3 cystatin-like domains.
- Db 252 GEDFL--PPMVCYGCPCPPIPVDSPDIEALUHSIAKLNAAENATPFKIDNPKKARYQV 309 RA This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
- Qy 63 AGKKYFDVVAETTCGSKESNEBELTESCTKLKGQDLCDAEVYYVPPWEEKRKYTPV 118 RA
- Db 310 CGGLKYSIVFVIAETTCGKGNSNEBELTSCTNHGQ1LHCDDANVYYVPPWEEKRKYTPV 365 RA
- RESULT 6 OC Mus musculus (Mouse). Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI TAXID=10090;
- ID_KNG_MOUSE STANDARD; PRT; 661 AA. RN
- AC Q08677; Q91XPS; 9Q1XPS; STRAIN=C57BL/6CBA; TISSUE=Liver; RC
- DT 16-OCT-2001 (Rel. 40, Created) DT
- DT 16-OCT-2001 (Rel. 40, Last sequence update) DE
- DE 15-MAR-2004 (Rel. 43, Last annotation update) DE
- GN Kininogen precursor [Contains: Bradykinin]. DE
- OS Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. OC
- RN ID_KNG_MOUSE STANDARD; PRT; 661 AA. RN
- SEQUENCE FROM N.A. (ISOFORMS HMW AND LMW). RN
- RECORD ID: Q08677-1; Sequence=Displayed; RN
- RECORD ID: Q08677-2; Sequence=VSP_001264; RN
- RECORD ID: 008677-1; Sequence=Placenta; RN
- RECORD ID: 008677-2; Sequence=Plasma; RN
- RECORD ID: 008677-3; Sequence=VSP_001264; RN
- RECORD ID: 008677-4; Sequence=VSP_001264; RN
- RECORD ID: 008677-5; Sequence=VSP_001264; RN
- RECORD ID: 008677-6; Sequence=VSP_001264; RN
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- RECORD ID: 008677-12; Sequence=VSP_001264; RN
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CC	NCBI_TAXID=10116;
RN	[1] SEQUENCE FROM N.A. (ISOFORMS HMW AND LMW).
RP	"Different expression patterns and evolution of the rat kininogen gene family.",
RX	Kitagawa H., Kitamura N., Hayashida H., Miyata T., Nakaniishi S.;
RA	EMBL; DR0435; BAA19743_1; -;
RT	DR EMBL; DBA415; BAA19742_1; -;
RL	DR EMBL; ARK005547; BAA224115_1; -;
RL	DR EMBL; BC018158; AAH18158_1; -;
RN	MGD: MGI:1097705; Rng.
DR	InterPro; IPR000010; Cystatin.
DR	InterPro; IPR002395; Kininogen.
PFam; PF00031; cystatin_3.	
PRINTS; PR0034; KININOCEN.	
SMART; SM0042; CY_3.	
PROSITE; PS00287; CYSTATIN_1.	
PROSITE; PS00287; CYSTATIN_1.	
KW	Glycoprotein; Plasma; Repeating; Thiol protease inhibitor; Vasodilator; Bradykinin; Blood coagulation; Inflammatory response; Signal; Alternative splicing.
FT	SIGNAL 1 18 POTENTIAL.
FT	CHAIN 19 661 KININOCEN.
FT	CHAIN 19 379 KININOCEN HEAVY CHAIN.
FT	CHAIN 380 388 BRADYKININ.
FT	CHAIN 389 661 KININOCEN LIGHT CHAIN.
FT	DOMAIN 19 135 CYSTATIN-LIKE 1.
FT	DOMAIN 136 257 CYSTATIN-LIKE 2.
FT	DOMAIN 258 379 CYSTATIN-LIKE 3.
FT	DOMAIN 439 524 HIS-RICH.
FT	DISULFID 28 631 INTERCHAIN (BY SIMILARITY).
FT	DISULFID 83 94 BY SIMILARITY.
FT	DISULFID 107 125 BY SIMILARITY.
FT	DISULFID 141 144 BY SIMILARITY.
FT	DISULFID 205 217 BY SIMILARITY.
FT	DISULFID 228 247 BY SIMILARITY.
FT	DISULFID 263 266 BY SIMILARITY.
FT	DISULFID 327 339 BY SIMILARITY.
FT	DISULFID 350 369 BY SIMILARITY.
FT	CARBODY 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBODY 168 168 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBODY 204 204 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBODY 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC 401 432 VSPPTIAREQDERATEQDPTGHGWLHEKQ -> RLLRA CBYKGRSLKAGAEAPERQAESSYKQ (in isoform LMW)
FT	/FTId=VSP_001263.
FT	VARSPLIC 433 661 Missing (in isoform LMW).
FT	/FTId=VSP_001264.
SQ	SEQUENCE 661 AA; 73102 MW; 774460258D58196E CRC64;
Query Match	60.1%; Score 413; DB 1; Length 661;
Best Local Similarity	66.7%; Pred; No. 1.1e-31;
Matches 78;	Conservative 11; Mismatches 28; Indels 0; Gaps 0;
CC	-!- SUBCELLULAR LOCATION: Secreted.
CC	-!- ALTERNATIVE PRODUCTS:
CC	Event=Alternative splicing; Named isoforms=2;
CC	Name=HMW;
CC	Isoid=P08934-1; Sequence=Displayed;
CC	Name=LMW;
CC	Isoid=P08934-2; Sequence=VSP_001265; VSP_001266;
CC	-!- TISSUE SPECIFICITY: Plasma.
CC	-!- PTM: Bradykinin is released from kininogen by plasma kallikrein.
CC	-!- MISCELLANEOUS: Rats express four types of kininogens: the classical HMW/LMW kininogens and two additional LMW-like kininogens: T-I and T-II.
CC	-!- SIMILARITY: Contains 3 cystatin-like domains.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	EMBL; L29428; AAA41486.1; -.
DR	DR

RESULT 7

KNG_RAT
ID RNG_RAT STANDARD; PRT; 639 AA.
AC P08933; P08933; 09, Created
DT 01-NOV-1998 (Rel. 09, Last sequence update)

DT 01-NOV-1988 (Rel. 09, Last annotation update)
DE Kininogen precursor [Contains: Bradykinin].
GN KNG.
OS Rattus norvegicus (Rat).

Eukaryota; Metzoa; Chordata; Craniata: Vertebrata; Euteleostomi:
Mammalia; Buteraria; Rodentia; Muridae; Murinae; Rattus.
OC

EMBL; M11984; AAA41487.1; -.	OX [1]
EMBL; M14369; AAA41484.1; -.	RN
DR EMBL; M14369; AAA41485.1; ALT_SEQ.	SEQUENCE FROM N.A.
DR EMBL; M16455; AAA41482.1; -.	RX MEDLINE-86008264; PubMed=2413018;
PIR; A25486; A25486.	RX
DR InterPro; IPR000010; Cystatin.	RA "Primary structures of the mRNAs encoding the rat precursors for bradykinin and T-kinin. Structural relationship of kininogens with major acute phase protein and alpha 1-cysteine proteinase inhibitor."
DR InterPro; IPR002395; Kininogen.	RT
DR PRINTS; PF00031; cystatin_3.	RT
DR SMART; SM00043; CY_3.	RT
DR PROSITE; PS00287; C1STATIN; 2.	CC as precursor of the active peptide bradykinin and they
DR Glycoprotein; Plasma; Repeat; Thiol protease inhibitor; Vasodilator; Bradykinin; Blood coagulation; Inflammatory response; Signal; Alternative splicing; Multigene family.	CC functions: (1) as precursor of the active peptide bradykinin and they play a role in blood
KW increase of vascular permeability. (2) They play a role in blood coagulation by helping to position optimally prekallikrein and factor XI next to factor XII. (3) They are inhibitor of thiol proteases.	CC
FT SIGNAL 1 18	CC SUBCELLULAR LOCATION: Extracellular.
FT CHAIN 19 639 KININGEN.	CC TISSUE SPECIFICITY: Plasma.
FT CHAIN 19 360 KININGEN. HEAVY CHAIN.	CC INDUCTION: In response to an inflammatory stimulant. T-kininogen
FT PEPTIDE 381 389 BRADYKININ.	CC T-1 synthesis is induced and the plasma concentration of T-kininogen 1 is raised.
FT CHAIN 390 639 KININGEN LIGHT CHAIN.	CC PTM: AS T-KININ IS PRECEDED BY A MET INSTEAD OF AN ARG OR LYS, IT IS NOT RELEASED FROM ITS PRECURSOR BY EITHER TISSUE OR PLASMA KALLIKREIN.
FT DOMAIN 19 136 CYSTATIN-LIKE 1.	CC MISCELLANEOUS: Rats express four types of kininogens: the classical HMW and LMW kininogens produced by alternative splicing of the same gene, and two additional LMW-like kininogens: T-I and T-II.
FT DOMAIN 137 258 CYSTATIN-LIKE 2.	CC
FT DOMAIN 259 380 CYSTATIN-LIKE 3.	CC
FT DOMAIN 439 514 HIS-RICH.	CC
FT DISULFID 28 609 INTERCHAIN (BY SIMILARITY).	CC
FT DISULFID 83 94 BY SIMILARITY.	CC
FT DISULFID 107 126 BY SIMILARITY.	CC
FT DISULFID 142 145 BY SIMILARITY.	CC
FT DISULFID 206 218 BY SIMILARITY.	CC
FT DISULFID 229 248 BY SIMILARITY.	CC
FT DISULFID 264 267 BY SIMILARITY.	CC
FT DISULFID 328 340 BY SIMILARITY.	CC
FT DISULFID 351 370 BY SIMILARITY.	CC
FT CARBOHYD 82 82 N-LINKED (GLCNAC. .) (POTENTIAL).	CC
FT CARBOHYD 127 127 N-LINKED (GLCNAC. .) (POTENTIAL).	CC
FT CARBOHYD 169 169 N-LINKED (GLCNAC. .) (POTENTIAL).	CC
FT CARBOHYD 205 205 N-LINKED (GLCNAC. .) (POTENTIAL).	CC
FT CARBOHYD 294 294 N-LINKED (GLCNAC. .) (POTENTIAL).	CC
FT CARBOHYD 529 529 N-LINKED (GLCNAC. .) (POTENTIAL).	CC
FT VARSPLIC 402 433 VPSYKSTARVQEEBERDPCNEOQPINGHGMWLRKQ -> RLIINS CEYKGRLKLKAGPAPERQEAESTVTP (in isoform LMW).	CC
FT VARSPLIC 434 639 Missing (in isoform LMW).	CC
PT CONFLICT 61 61 /FTId=vSP_001265.	DR /FTId=vSP_001265.
PT CONFLICT 63 70933 MW E -> K (IN REF. 2).	DR SMART; SM00043; CY_3.
SQ CONFLICTE 639 AA; D3172DP4FF5GAF5 CRC64;	DR PROSITE; PS00287; C1STATIN; 2.
DB GDDLFELPEDPGCPRNIPVDSPLEKAQLGHSLAQLNANNHTFYFKDTVKATSQV 312	KW GLYCOPROTEIN; Plasma; Reheat; Vasodilator; Multigene family; Thiol protease inhibitor; Bradykinin; Acute phase; Signal.
Query Match 59.7% Score 410; DB 1; Length 639;	FT SIGNAL 1 18
Best Local Similarity 66.4%; Pred. No. 2e-31; Indels 0; Gaps 0;	FT CHAIN 19 430 KININGEN. T-II.
Matches 77; Conservative 13; Mismatches 26;	FT CHAIN 19 375 HEAVY CHAIN.
Qy 3 GKDFFVQOPTKICVGCPRDIPNTNSPELEETLTITKLNAAANNATFYKIDNVKARVOVY 62	FT PEPTIDE 376 386 T-KININ.
Db 253 GDDLFFELPEDPGCPRNIPVDSPLEKAQLGHSLAQLNANNHTFYFKDTVKATSQV 312	FT CHAIN 387 430 LIGHT CHAIN.
Qy 63 AGKKYFIDFVARETTCSKEEELTESCETKLGOSLDNAEVTYVWPWKKIFTY 118	FT DOMAIN 19 135 CYSTATIN-LIKE 1.
Db 313 AGTKYVTFIARETKCSKEEALTAADCETKLGOSLNCAVNPWNKVVSTV 368	FT DOMAIN 136 257 CYSTATIN-LIKE 2.
RESULT 8	FT DOMAIN 258 375 CYSTATIN-LIKE 3.
KNT2_RAT ID KNT2_RAT STANDARD; PRT; 430 AA.	FT DISULFID 28 404 INTERCHAIN (BY SIMILARITY).
AC P08937; 09, Created	FT DISULFID 83 94 BY SIMILARITY.
DT 01-NOV-1998 (Rel. 09, Last sequence update)	FT DISULFID 327 339 BY SIMILARITY.
DT 15-MAR-2004 (Rel. 43, Last annotation update)	FT DISULFID 350 369 BY SIMILARITY.
DE (Thiotokinogen II precursor (Major acute phase protein) (Alpha-1-NAP) (Contains: T-kinin).	FT CARBOHYD 82 82 N-LINKED (GLCNAC. .) (POTENTIAL).
DE Rattus norvegicus (Rat).	FT CARBOHYD 126 126 N-LINKED (GLCNAC. .) (POTENTIAL).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	FT CARBOHYD 168 168 N-LINKED (GLCNAC. .) (POTENTIAL).
OC	FT CARBOHYD 204 204 N-LINKED (GLCNAC. .) (POTENTIAL).
SEQUENCE 430 AA; 47524 MW; 43EDF02D1BF55076 CRC64;	SQ 430 AA; 47524 MW; 43EDF02D1BF55076 CRC64;
Query Match 56.5%; Score 388; DB 1; Length 430;	Query Match

FT CONFLICT 414 414 R -> G (IN REF. 2 AND 3).
 FT CONFLICT 415 415 A -> L (IN REF. 2).
 FT CONFLICT 420 421 DH -> ER (IN REF. 3).
 FT CONFLICT 430 430 P -> S (IN REF. 1).
 SQ SEQUENCE 430 AA: 47715 MW: FAEBB78FAF4723C3 CRC64;

Query Match 55.3%; Score 380; DB 1; Length 430;
 Best Local Similarity 62.1%; Pred. No. 9e-29;
 Matches 72; Conservative 14; Mismatches 30; Indels 0; Gaps 0;

Qy 3 GKDVFQPPTKICVGCPDTPNSPELELTITKUNAENNATYFKIDNPKKARVQVVA 62
 Db 252 GDDLFELLPKNCRGCPREPVDSPELKEALGHSIAQLNAQINHIFPKIDTVKGATQSQQV 311

RESULT 10
 CYTF_MOUSE STANDARD PRT; 145 AA.
 AC CB9058; ID CYTF_HUMAN STANDARD; PRT; 145 AA.
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cystatin F precursor (Leukocystatin) (Cystatin 7) (Cystatin-like protein)
 DE metastasis-associated protein (CMAP).
 GN CST7.
 OS Mus musculus (Mouse).
 OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Bacteria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98298157; PubMed=9733783;
 RA Halfon S., Ford J., Foster J., Dowling L., Lucian L., Sterling M.,
 RA Xu Y., Weiss M., Ikeda M., Liggett D., Helms A., Caux C., Lebecque S.,
 RA Hannum C., Menon S., McClanahan T., Gorman D., Zurawski G.;
 RT "Leukocystatin, a new class II cystatin expressed selectively by
 RT hematopoietic cells.",
 RL J. Biol. Chem. 273:16400-16408 (1998).
 CC FUNCTION: Inhibits papain and cathepsin L but with affinities
 lower than other cystatins. May play a role in immune regulation
 through inhibition of a unique target in the hematopoietic system.
 CC !- SUBCELLULAR LOCATION: Secreted (Probable).
 CC !- SIMILARITY: Belongs to the cystatin family.

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CC DR EMBL; AP031826; AAC4140_1; -.
 DR HSSP; P01034; IGF6; -.
 DR MGI; MGI:1229217; Cct7.
 DR InterPro; IPR000010; Cystatin.
 DR Pfam; PF00031; Cystatin; 1.
 DR SMART; SM00043; CY1.
 DR PROSITE; PS00287; CSTATIN; FALSE NEG.
 KW Thiol protease inhibitor; Glycoprotein; Signal.

FT SIGNAL 1 18 POTENTIAL CYSTATIN F.
 FT CHAIN 19 144 CYSTATIN F.
 FT ACT SITE 36 36 REACTIVE SITE.
 FT SITE 80 84 SECONDARY AREA OF CONTACT.
 FT DISULFID 98 109 BY SIMILARITY.
 FT DISULFID 123 143 BY SIMILARITY.
 SQ SEQUENCE 144 AA: 16380 MW: B5837334C1BA89C CRC64;

Query Match 25.0%; Score 171.5; DB 1; Length 144;
 Best Local Similarity 35.5%; Pred. No. 1.7e-09;
 Matches 39; Conservative 22; Mismatches 42; Indels 7; Gaps 3;

Qy 4 KDFYQPPTKICVGCPDTPNSPELELTITKUNAENNATYFKIDNPKKARVQVVA 63
 Db 27 KD1I--SSVQGPKPETTNPAVLKARHSVSKFNCTNDFLFKEVSVERALYVVK 83

Qy 64 GKXYFIDFYARETTCSKESNEELTESCTRKLGOSLDCNAAEVVVVPEKKIYPTV 110
 Db 84 GLKYMLEVKGIGRATICRKTMMHHOL-DNCDFTQTNPALKETLYCYSEVWVTPW 132

RESULT 11
 CYTF_HUMAN STANDARD; PRT; 145 AA.
 AC O76096; Q9UED4;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-OC-2003 (Rel. 42, Last annotation update)
 DE Cystatin F precursor (Leukocystatin) (Cystatin 7) (Cystatin-like protein)
 DE metastasis-associated protein (CMAP).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TAXID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98406133; PubMed=9733783;
 RA Ni J., Fernandez M.A., Danielsson L., Chillakuru R.A., Zhang J.,
 RA Grabb A., Su J., Gentz R., Abramhamson M.;
 RT "Cystatin F is a Glycosylated human low molecular weight cysteine proteinase inhibitor.",
 RT J. Biol. Chem. 273:24797-24804 (1998).
 RL [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=98298157; PubMed=9632704;
 RA Halfon S., Ford J., Foster J., Dowling L., Lucian L., Sterling M.,
 RA Xu Y., Weiss M., Ikeda M., Liggett D., Helms A., Caux C., Lebecque S.,
 RA Hannum C., Menon S., McClanahan T., Gorman D., Zurawski G.;
 RT "Leukocystatin, a new class II cystatin expressed selectively by
 RT hematopoietic cells.",
 RL J. Biol. Chem. 273:16400-16408 (1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Morita M., Arakawa H., Yoshiuchi N.;
 RA "Human homologue of murine CMAP."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20399571; PubMed=10945474;
 RA Morita M., Hara Y., Tamai Y., Arakawa H., Nishimura S.;
 RT "Genomic construct and mapping of the gene for CNAP (Leukocystatin)/Cystatin F, CS17) and identification of a proximal novel gene, BSCv (C2orf3).";
 RT Genomics 67:87-91 (2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21338719; PubMed=11780052;
 RA Deloucas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard D.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakley S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrell W.D., Butler A.P., Carter C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Cleo C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Franklin J.A., French L., Fraser P., Garner P.,
 RA Grahame D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., Knights A., Laird G.K., Lawlor S.,

8 QPPTRKICVGCPDRDPTNSPELEELTHTTKLNAENNATFYKIDNVKKARVQVAGKKY 67
 RT inhibitor that is a target for cross-linking by transglutaminase.;"
 RL J. Invest. Dermatol. 116:693-701 (2001).
 CC -|- FUNCTION: Shows moderate inhibition of cathepsin B but is not
 active against cathepsin C.
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- TISSUE SPECIFICITY: Restricted to the stratum granulosum of normal
 skin, the stratum granulosum/spinosum of porotic skin, and the
 secretory coils of eccrine sweat glands. Low expression levels are
 found in the nasal cavity.
 CC -|- PTM: Substrate for transglutaminases. Acts as an acyl acceptor but
 CC not as an acyl donor.
 CC -|- SIMILARITY: Belongs to the cystatin family.
 CC -|- RESULT 13
 CYTM_HUMAN STANDARD; PRT; 149 AA.
 ID CYTM_HUMAN STANDARD;
 AC 015828;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cystatin M precursor (Cystatin E).
 GN CSM16.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI TaxID=9606;
 RN [1] PSEQUENCE FROM N.A.
 RX MEDLINE=97150844; PubMed=895380;
 RA Ni J., Abrahamsen M., Zhang M., Hernandez M.A., Grubb A., Su J.,
 RA Yu G.L., Li Y., Parmalee D., Xing L., Coleman T.A., Gentz S.,
 RA Thotakura R., Nguyen N., Hesselborg M., Gentz R.;
 RT "Identification, cloning, and characterization of cystatin M, a novel
 cysteine proteinase inhibitor, down-regulated in breast cancer.",
 RL J. Biol. Chem. 272:903-910(1997).
 [2] PSEQUENCE FROM N.A.
 RX MEDLINE=97256812; PubMed=9099741;
 RA Ni J., Abrahamsen M., Hernandez M.A., Grubb A., Su J.,
 RA Yu G.L., Li Y., Parmalee D., Xing L., Coleman T.A., Gentz S.,
 RA Thotakura R., Nguyen N., Hesselborg M., Gentz R.;
 RT "Cystatin E is a novel human cysteine proteinase inhibitor with
 structural resemblance to family 2 cystatins.",
 RL J. Biol. Chem. 272:10853-10858(1997).
 [3] PSEQUENCE FROM N.A.
 RX TISSUE=Prostate; PubMed=12477932;
 RX MEDLINE=22388257;
 RA Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collings F.S., Wagner L., Schuler G.D.,
 RA Altschuler S.F., Zeeberg B., Bustow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong I.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Yoshiyuki S., Carninci P., Prange C.,
 RA Baha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEvany P.J., McKernan K.J., Malek J.A., Gunaratne P.R.,
 RA Richards A., Worley K.C., Hale S., Garcia A.M., Hale J.J., Hulyk S.W.,
 RA Villalon D.K., Muzyk D.M., Soderberg R.J., Liu X., Gibbs R.A.,
 RA Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
 RA Buttefield Y.S.N., Krzywinski M.T., Skalska U., Smalius D.B.,
 RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.",
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [4] CHARACTERIZATION, AND TISSUE SPECIFICITY.
 RX MEDLINE=21246810; PubMed=11318457;
 RA Zeeuw P.L., van Wijnen-Willems I.M., Janssen B.J., Sotiropoulos G.,
 RA Curns J.H., Meis J.H., Janssen J.J., van Ruissen P., Schalkwijk J.,
 RT "Cystatin M/E expression is restricted to differentiated epidermal
 keratinocytes and sweat glands: a new skin-specific proteinase
 RN

RT inhibitor that is a target for cross-linking by transglutaminase.;"
 RL J. Invest. Dermatol. 116:693-701 (2001).
 CC -|- FUNCTION: Shows moderate inhibition of cathepsin B but is not
 active against cathepsin C.
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- TISSUE SPECIFICITY: Restricted to the stratum granulosum of normal
 skin, the stratum granulosum/spinosum of porotic skin, and the
 secretory coils of eccrine sweat glands. Low expression levels are
 found in the nasal cavity.
 CC -|- PTM: Substrate for transglutaminases. Acts as an acyl acceptor but
 CC not as an acyl donor.
 CC -|- SIMILARITY: Belongs to the cystatin family.
 CC -|- RESULT 14
 CYTM_BOVIN STANDARD; PRT; 148 AA.
 ID CYTM_BOVIN STANDARD;
 AC P01035;
 DT 21-JUL-1986 (Rel. 01, Created)
 AC P01035;
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 AC P01035;
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cystatin C precursor (Colostrom thiol proteinase inhibitor).
 OS Bos taurus (Bovine).
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Ruminantia; Bovoidea;
 OC Bovidae; Bovines; Bos.
 NCBI_TAXID=9913;
 [1] SEQUENCE FROM N.A., SEQUENCE OF 66-83, AND CHARACTERIZATION.
 RN TMMGSTDCRKTRVTGDHVDLT-TCPZLAAQQEKLRCDFEVLYVWQ
 RT TISSUE=Cerebrospinal fluid, and Choroid plexus;

MEDLINE=98094199; PubMed=9434110;
 RA Olson S.-L., Ek B., Wilm M., Broberg S., Rask L., Bjoerk I.;
 RT "Molecular cloning and N-terminal analysis of bovine cystatin C
 identifier of a full-length N-terminal region.",
 RL Biochim. Biophys. Acta 1343:203-210(1997).
 RN [2]
 SEQUENCE OF 37-148
 MEDLINE=95231205; PubMed=3801407;
 RX Hirado M., Tsunashima S., Satiyama F., Niinobe M., Fujii S.;
 RT "Complete amino acid sequence of bovine colostrum low-Mr cysteine
 proteinase inhibitor.",
 RT FEBS Lett. 186:41-45(1985).
 RL CC !- FUNCTION: This is a thiol proteinase inhibitor.
 CC !- MASS SPECTROMETRY MW=11420; METHD=MDI.
 CC !- SIMILARITY: Belongs to the cystatin family.
 CC EMBL; AJ242926; CAB67543; 1; -
 DR InterPro; IPR000010; Cystatin.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 or send an email to license@isb-sib.ch).
 CC DR InterPro; IPR001363; Fetuin.
 CC PFAM; PF00031; cystatin; 2.
 CC SMART; SM0003; Cy; 2.
 CC PROSITE; PS01254; FETUIN_1; 1.
 CC PROSITE; PS01255; FETUIN_2; 1.
 CC GLYCOPROTEIN; Signal; Repat.
 CC KW SIGNAL AA: 1 18
 FT SIGNAL 1 18
 FT CHAIN 19 378
 FT DOMAIN 27 152
 DR DOMAIN 153 273
 FT DISULFID 96 107
 FT DISULFID 120 140
 FT DISULFID 154 157
 FT DISULFID 217 224
 FT DISULFID 237 260
 FT CARBOHYD 40 40
 FT CARBOHYD 139 139
 SQ SEQUENCE 378 AA: 41532 MW: 0660A5C3B03C978 CRC64;
 Query Match 19.7%; Score 135; DB 1; Length 378;
 Best Local Similarity 25.8%; Pred. No. 1.5e-05;
 Matches 33; Conservative 32; Mismatches 49; Indels 14; Gaps 5;

QY 7 VQPPTK----IVCGCPRDIPNNSPEELBTLTHTITKLNAENNATYFKIDNVKKRQVQV 61
 Db 142 LRPVSKRKIHSMPDCDPFDVLDISAPSVLEATESLAKFNSENPSKQYALV KVTKTATTQW 200
 QY 24 NSPEELBTLTHTITKLNAENNATYFKIDNVKKRQVQVAGKKYFLDFVARETTCSKEEN 83
 Db 62 VAGKKYFLDFVARETTCSKEENELTSCETKLGQSLLDCNAEVVYVPW--EKKIVPVT 119
 QY 48 NEEGVDEALSFAVSEPNKNSDAYQSRVTVVRKQVNSMFLDVEIGRTOTK-S 105
 Db 201 VVSPSYFVEYLKESPTQSDCSLQLSDSEPVGL--CQGSLLIKSPGPVPPQRFKKVT 257
 QY 120 VNHWECEP 127
 Db 258 VS---CEP 262

Search completed: September 24, 2004, 14:09:13
 Job time : 9.636 secs

RESULT 15
 FETB_RAT STANDARD PRT; 378 AA.
 ID FETB_RAT STANDARD PRT; 378 AA.
 AC Q9QX79; (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 GN FETUB.
 OS Rattus norvegicus (Rat).
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TAXID=10116.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN Sprague-Dawley; TISSUE=liver;
 RC MEDLINE=1047975;
 RA Olivier E., Soury E., Ruminy P., Russouw A., Parmentier F., Daveau M.,
 RA Salier J.-P.;
 RA "Fetuin-B, a second member of the fetuin family in mammals.";



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OM protein - protein search, using sw model

Run on: September 24, 2004, 14:06:08 ; Search time 13:716 Seconds
(without alignments)

Title: US-10-661-784-3

Perfect score: 687

Sequence: 1 GSGKDFQPPPTKICVGCPRD.....VPWEEKIYPTVTVNHWECEP 127

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters:

283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : PIR78:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

% Query

Result No. Score

Match Length DB ID

				Description
-	1	618	90.0	KGHU1 kininogen, LMW pre
	2	618	90.0	KGHUH1 kininogen, HMW Pre
	3	440	64.0	KGBOH1 kininogen, LMW I P
	4	440	64.0	KGBOL1 kininogen, HMW II P
	5	413	60.1	KGBOL2 kininogen, HMW II K
	6	410	59.7	A28055 kininogen, HMW I
	7	410	59.7	A28486 kininogen, HMW I P
	8	388	56.5	A23897 major acute phase T-kininogen, LMW I
	10	388	56.5	B28055 major acute phase T-kininogen I
	11	381	55.5	A28793 bovine cystatin C precursors
	12	380	55.3	A36163 bovine cystatin C precursors
	13	327.5	20.0	B29632 bovine cystatin C precursors
	14	132.5	19.3	B29633 bovine cystatin C precursors
	15	130	18.9	BUDCH bovine cystatin C precursors
	16	129	18.8	S07085 bovine cystatin C - rat
	17	128	18.6	S10587 bovine cystatin C precursors
	18	124.5	18.6	A36163 bovine cystatin C precursors
	19	124.5	18.1	A36164 bovine cystatin C precursors
	20	110.5	17.2	B29632 bovine cystatin C precursors
	21	113	16.4	JQ1470 bovine cystatin C precursors
	22	112	16.3	S68034 bovine cystatin C precursors
	23	112	16.3	S68035 bovine cystatin C precursors
	24	111	16.2	JC2040 bovine cystatin C precursors
	25	109.5	15.9	UDHUP2 bovine cystatin C precursors
	26	108.5	15.8	UDHUP1 bovine cystatin C precursors
	27	107	15.6	T33740 bovine cystatin C precursors
	28	106	15.4	JC4918 bovine cystatin C precursors
	29	105.5	15.4	A43428 bovine cystatin C precursors

30	102	14.8	122	2 A43644 sarcocystatin A precursor
31	101.5	14.8	133	2 JC4536 cystatin IR - maize
32	97.5	14.2	135	2 JC4007 cystatin D precursor
33	97	14.1	142	2 A47142 hypothetical prote
				alpha-2-HS-glycoprotein-related peptide
				cystatin - avocatin
				cysteine proteinas
				sercain precursor -
				cysteine proteinas
				cystatin - maize
				cystatin - field m
				alpha-2-HS-glycoprotein-dependent lip
				Ca2+ dependent lip

ALIGNMENTS

RESULT 1				
KGHU1 kininogen, LMW precursor [validated] - human				
N:Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen I; kininogen I; prokininogen				
N:Contains: bradykinin (kallidin); kininogen I; prokininogen				
C:Species: Homo sapiens (man)				
C:Date: 06-Jul-1982 #sequence revision 27-Nov-1985 #text change 08-Dec-2000				
C:Accession: A01280; B25226; A27900; A27999; A31905; A34030				
R:Ohkubo, I.; Kurachi, K.; Takasawa, T.; Shiozawa, H.; Sasaki, M.				
J. Biol. Chem. 23, 5691-5697, 1984				
Biochemistry 23, 5691-5697, 1984				
A:Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its identity				
A:Reference number: A90490; MUID: 85122621; PMID: 6441591				
A:Accession: A01280				
A:Molecule type: mRNA				
A:Residues: 1-427 <OKX>				
A:Cross-references: CB:K02566; NID:G17789; PIDN:AAA35497.1; PID:9177890				
R:Takagaki, Y.; Kitamura, N.; Nakanishi, S.				
J. Biol. Chem. 260, 8601-8609, 1985				
A:Title: Cloning and sequence analysis of cDNAs for human high molecular weight and low molecular weight kininogens				
A:Reference number: A22544; MUID: 85224582; PMID: 299293				
A:Accession: B22526				
A:Molecule type: mRNA				
A:Residues: 1-427 <TAK>				
A:Cross-references: GB:MM11437; NID:G186751; PIDN:ABA59551.1; PID:9386853				
R:Lottschied, P.; Kellermann, J.; Heischner, A.; Rauth, G.; Mueller-Esterl, W.				
in Kinins IV - part A, Greenbaum, L.M., and Margoliash, H.S., eds., pp.91-95, Plenum, New York, 1985				
A:Title: Amino acid sequence of the light chain of human low molecular mass kininogen.				
A:Accession: A27900				
A:Molecule type: protein				
A:Residues: 390-427 <LOT>				
R:Mindrou, T.; Carretero, O.A.; Proud, D.; Walz, D.; Scicli, A.G.				
Biochem. Biophys. Res. Commun. 152, 519-526, 1988				
A:Title: A new kinin moiety in human plasma kininogens.				
A:Reference number: A27699; MUID: 88209021; PMID: 3365237				
A:Accession: A27699				
A:Molecule type: protein				
A:Residues: 380-389 <MINN>				
R:Kato, H.; Matsunaga, Y.; Kato, H.				
J. Biol. Chem. 263, 16051-16054, 1988				
A:Title: Purification and identification of [hydroxyprolyl(3)]bradykinin in ascitic fluid.				
A:Reference number: A31905; MUID: 89034061; PMID: 3182782				
A:Accession: A31905				
A:Molecule type: protein				
A:Residues: 381-389 <MALE>				
R:Sasaguri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K.				
Biochem. Biophys. Res. Commun. 150, 511-516, 1988				
A:Title: Identification of [hydroxyproline(3)-lysyl]-bradykinin released from human platelets.				
A:Reference number: A34030; MUID: 88106632; PMID: 88209021				
A:Accession: A34030				
A:Molecule type: protein				
A:Residues: 380-389 <SAS>				

- R; Kitamura, M.; Kitagawa, H.; Fukushima, D.; Takagaki, Y.; Miyata, T.; Nakanishi, S.
 J. Biol. Chem. 260, 860-8617, 1985
 A; Title: Structural organization of the human kininogen gene and a model for its evolution
 A; Reference number: A95245; PMID:2989294
 A; Contents: annotation; gene organization
 R; Pierce, J. V.
 Fed. Proc. 27, 52-57, 1968
 A; Title: Structure of plasma kinins and kininogens.
 A; Reference number: A91455; PMID:90255622;
 A; Cross-references: GDB:125256; OMIM:228960
 A; Map position: 3q27-3q27
 A; Introns: 65/3; 102/3; 131/1; 18/3; 224/3; 253/1; 310/3; 346/3; 375/3; 401/3
 C; Superfamily: kininogen; cystatin homology <CY3>
 C; Comment: The LMW kininogen precursor is produced from the same gene as the HMW form (see above).
 C; Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of the alternative splicing; blood coagulation; cysteine proteinase inhibitor; glycine-rich region is present in the kininogen prior to the release of bradykinin.
 C; Genetics:
 A; Gene: GDB:KNG
 A; Cross-references: GDB:125256; OMIM:228960
 A; Map position: 3q27-3q27
 A; Introns: 65/3; 102/3; 131/1; 18/3; 224/3; 253/1; 310/3; 346/3; 375/3; 401/3
 C; Superfamily: kininogen; cystatin homology <CY3>
 C; Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; glycine-rich region is present in the kininogen prior to the release of bradykinin.
 P; 1-18/Domain: signal sequence #status predicted <SIG>
 P; 1-9-42/Domain: product: LMW prokininogen (kininogen I) #status predicted <MAT>
 P; 1-389/390-47/Product: LMW kininogen II #status predicted <MAT2>
 P; 1-9-31/Domain: cystatin homology <CY1>
 P; 142-253/Domain: cystatin homology CY2>
 P; 264-315/Domain: cystatin homology <CY3>
 P; 380-389/Product: lysyl-bradykinin (kallidin II) #status experimental <BDY>
 P; 381-389/Product: bradykinin (kallidin I) #status experimental <BDY>
 P; 390-427/Product: LMW kininogen light chain #status experimental <LCH>
 P; 1.9/Modified site: pyroglutamyl carboxylic acid (Gln) (in mature form) #status predicted
 P; 142-145/206-218/229-248, 264-267, 328-340/351-370/Disulfide bonds:
 P; 148-159/205-214/Binding site: carbohydrate (Asn) (covalent) #status predicted
 P; 379-380/Cleavage site: Met-Lys (kallikrein) #status experimental
 P; 383/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental
 P; 389-390/Cleavage site: Arg-Ser (kallikrein) #status experimental
 P; 401/Binding site: carbohydrate (Tyr) (covalent) #status absent
 Query MatchScore 90.0%; Score 618; DB 1; Length 427;
 Best Local Similarity 100.0%; Pred. No. 3-6e-50;
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
- Qy 3 GKDFFQOPTKTCVGCPPDIPNTSPPEETLTHTTKLNAAANNATYFKDNVKKARQVTV 62
 Db 253 GKDFFQOPTKTCVGCPPDIPNTSPPEETLTHTTKLNAAANNATYFKDNVKKARQVTV 312
 Qy 63 AGKKYFIDFVAEETCSKEESNLSECEPKLGQSLDCAEVTVTPWEEKKIYPTV 118
 Db 313 AGKKYFIDFVAEETCSKEESNLSECEPKLGQSLDCAEVTVTPWEEKKIYPTV 368
- RESULT 2
 KGHHUH
 kininogen, HMW precursor [validated] - human
 N; Alternative names: alpha-2-thiol proteinase inhibitor; preprokininogen; prokininogen
 N; Contains: bradykinin (kallidin I); HMW kininogen I; low molecular weight
 C; Species: Homo sapiens (man)
 C; Accession: A01279; A25276; A9153; A24871; A27899; A31905; A34030; S02
 R; Ohkubo, I.; Kurachi, K.; Takasawa, T.; Shiozawa, H.; Sasaki, M.
 Biochemistry 23, 5691-5697, 1984
 A; Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its identification
 A; Reference number: A90450; PMID:85122621; PMID:6441551
 A; Molecule type: mRNA
 A; Residues: 1-389 <OKH>
 A; Cross-references: GB:K02566; NID:9177889
 R; Takegaki, Y.; Kitamura, N.; Nakanishi, S.
 J. Biol. Chem. 260, 8601-8609, 1985
 A; Title: Cloning and sequence analysis of cDNAs for human high molecular weight and low
 A; Reference number: A92544; PMID:85234582; PMID:93223854; PMID:93223854; PMID:8467916
 A; Accession: A25276
 A; Molecule type: protein
 A; Residues: 380-389 <OKAT2>
 A; Experimental source: urine
 A; Note: this peptide had Pro-383 modified to 4-hydroxyproline
 A; Accession: B61495
 A; Molecule type: protein
 A; Residues: 381-389 <OKAT2>

RESULT 3						
Qy	3	GKDFVQPPTRKICVGCPRDIPNTNSPELEETLTITKLNAENNATFYKIDVYKKARVQQV	62	KGB011		
Db	253	GDFTVQPPTRKICVGCPRDIPNTNSPELEETLTITKLNAENNATFYKIDVYKKARVQQV	312	N;Altermate names: alpha-2-thiol proteinase inhibitor; preprokininogen N;Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen C;Species: Bos primigenius taurus (cattle)		
Qy	63	AGKCFIDFVARETCSKESNEELTSSCETKLGQSILDCCNAEVYVWEEKLYPTV	118	C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun-1999		
Db	313	AGKCFIDFVARETCSKESNEELTSSCETKLGQSILDCCNAEVYVWEEKLYPTV	368	C;Accession: A01283		
A;Title: Primary structures of bovine liver low molecular weight kininogen pre A;Reference number: A93984; MUID:83117859; PMID:6572010						
A;Accession: A01283						
A;Molecule type: mRNA						
A;Residues: 1-36 <NAA>						
A;Cross-references: GB:J00010; GB:V00426; NID:9163256; PID:AAA306041; PID:G19						
C;Comment: The LMW kininogen precursor is produced from the same gene as the F						
C;Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of blood coagulation; released from kininogen by kallikrein, is a potent vasoconstrictor.						
C;Comment: Bradykinin, released from kininogen by kallikrein, prior to the release of bradykinin						
C;Superfamily: kininogen, cystatin homology						
C;Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor						
F;1-18/Domain: signal sequence #status predicted <IG>						
F;19-436/Product: LMW kininogen I #status predicted <MAT>						
F;19-378/Product: LMW kininogen I heavy chain #status predicted <HCH>						
F;19-130/Domain: cystatin homology <CY1>						
F;141-252/Domain: cystatin homology <CY2>						
F;263-374/Domain: cystatin homology <CY3>						
F;379-388/Product: lysyl-bradykinin (kallidin II) #status predicted <KBDY>						
F;380-388/Product: bradykinin (kallidin I) #status predicted <BDY>						
F;389-436/Product: LMW kininogen I light chain #status experimental <LCH>						
F;19/Modified site: Pyrrolidine carboxylic acid (Gln) (in mature form) #status predicted <MAT>						
F;27-106/82-93/106-125/141-144/205-217/228-247/263-266/327-339/350-369/Disulfuride						
F;47-87/165-197/204/Binding site: carbonyl group (Asn) (covalent)						
F;378-379/Cleavage site: Met-Lys (kallikrein) #status predicted						
F;382/Modified site: 4-hydroxyproline (Pro) #status predicted						
F;388-389/Cleavage site: Arg-Ser (kallikrein) #status predicted						
Query Match 64.0% Score 440; DB 1; Length 436;						
Best Local Similarity 70.4%; Pred. No. 1; jhe-33;						
Matches 81; Conservative 14; Mismatches 20; Indels 0; Gaps 0						
Qy 4 KDFVQPPTRKICVGCPRDIPNTNSPELEETLTITKLNAENNATFYKIDVYKKARVQQV	63	KGB011				
Db 253 KDFVQPPTRKICVGCPRDIPNTNSPELEETLTITKLNAENNATFYKIDVYKKARVQQV	312	N;Altermate names: alpha-2-thiol proteinase inhibitor; preprokininogen N;Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen C;Species: Bos primigenius taurus (cattle)				
C;Accession: A01281; A91923; A91938; P29559						
R;Kitama, N., Sakaguchi, Y., Furuto, S.; Tanaka, T.; Nawa, H.; Nakaniishi, S., Nature 305, 545-549, 1983						
A;Title: A single gene for bovine high molecular weight and low molecular weight kininogen, HMW I precursor - bovine						
RESULT 4						
KGB011						
N;Altermate names: alpha-2-thiol proteinase inhibitor; preprokininogen N;Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen C;Species: Bos primigenius taurus (cattle)						
C;Accession: A01281; A91923; A91938; P29559						
R;Kitama, N., Sakaguchi, Y., Furuto, S.; Tanaka, T.; Nawa, H.; Nakaniishi, S., Nature 305, 545-549, 1983						
A;Title: A single gene for bovine high molecular weight and low molecular weight kininogen, HMW I precursor - bovine						

A:Accession: A01281 A:Molecule type: mRNA A:Residues: 1-621 <KIT> A:Cross-references: GB:V01491; GB:K01757; NID:9491; PID:CAA24735.1; PMID:9492 R:Fato, H.; Nagasawa, S.; Suzuki, T. J.: Biochem. 67, 313-322, 1970 A:Title: Studies on the structure of bovine kininogen: cleavages of disulfide bonds and A:Reference number: A91923; MUID:70160420; PMID:4986212 A:Accession: A91923 A:Molecule type: protein A:Residues: 378-393 <KIT> R:Han, Y.N.; Komiyama, M.; Iwanaga, S.; Suzuki, T. J.: Biochem. 77, 55-68, 1975 A:Title: Studies on the primary structure of bovine high-molecular-weight kininogen. Ami A:Reference number: A91938; MUID:7510265; PMID:1169237 A:Accession: A91938 A:Molecule type: protein A:Residues: 58-498 <HAN> R:Sueyoshi, T.; Miyata, H.; Hashimoto, N.; Kato, H.; Hayashida, H.; Miyata, T.; Iwanaga, J.: Biol. Chem. 262, 2768-2779, 1987 A:Title: Bovine high molecular weight kininogen. The amino acid sequence, positions of c A:Reference number: A92627; MUID:87137530; PMID:3546295 A:Molecule type: protein A:Residues: 'Z', 20-123, 'I', 125-127, 'I', 129-378 <SUB> R:JolitzBeisch, F.; Keilermann, J.; Hanschen, A.; Poertsch, B.; Muller-Esterl, W. Eur. J. Biochem. 152, 307-314, 1985 A:Title: The amino acid sequence of the light chain of human high-molecular-mass kininog A:Reference number: A91153; MUID:861030270; PMID:4054110 A:Contents: annotation; bovine cleavage sites; bovine carbohydrate binding sites R:Sueyoshi, T.; Miyata, H.; Iwanaga, S. Seikagaku 56, 808, 1984 A:Title: Disulfide bonds in bovine HMW kininogens. A:Reference number: A94300 A:Contents: annotation; disulfide bonds A:Note: article in Japanese C:Comment: The HMW kininogen precursor is produced from the same gene as the LMW form as C:Comment: Kininogen is a cysteine protease inhibitor, takes part in initiation of the C:Comment: The glycine/histidine/lysine-rich region of HMW kininogen light chain is impo C:Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, i C:Superfamily: Kininogen; cystatin homology C:Keywords: alternative splicing; blood coagulation; blood coagulation; bovine carbohyd F:1-18/Domain: cystatin homology <CY1> F:19-130/Domain: cystatin homology <CY2> F:141-252/Domain: cystatin homology <CY3> F:379-388/Product: lysyl-bradykinin (kallidin III) #status experimental <KBDY> F:380-388/Product: bradykinin (kallidin I) #status experimental <BDY> F:417-488/Region: glycine/histidine/lysine-rich F:19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen F:87-168, 169, 204/Binding site: carbohydrate (Asn) (covalent) #status experimental F:116/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental F:117/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental F:378-389/Cleavage site: Met-Lys (kallikrein) #status experimental F:388-389/Modified site: 4-hydroxyproline (Pro) #status predicted F:398-406, 512/Binding site: carbohydrate (Ser) (covalent) #status experimental F:438-499/Cleavage site: Arg-Thr (kallikrein) #status experimental	Qy 64 GKKFIDFVARETTCSKSNEELTESCTEKLQGSLDNNAEVVPPWERKTYPTV 118 Db 313 GLKYSIVVFARETTCSKSNEELTKSCSCEINHQILCDANVVVPWEEKVYPTV 367
RESULT 5	
KGBD12 kininogen, LMW II precursor - bovine N:Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen N:Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen C:Species: Bos primigenius taurus (cattle) C:Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 C:Accession: A01284 C:Cross-references: GB:V00427; PID:CAA23710.1; PMID:9490	
C:Comment: The LMW kininogen precursor is produced from the same gene as the HMW form as C:Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of the C:Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, i C:Comment: Proxyproline residue is present in the kininogen prior to the release of bradykinin. C:Superfamily: Kininogen; cystatin homology C:Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; glyc F:1-18/Domain: signal sequence #status predicted <SIG> F:19-377/Product: LMW kininogen II #status predicted <MAT> F:19-377/Binding site: Arg-Ser (kallikrein) #status predicted F:19-377/Domain: cystatin homology <CY1> F:141-252/Domain: cystatin homology <CY2> F:379-388/Product: bradykinin (kallidin III) #status experimental <KBDY> F:380-388/Product: bradykinin (kallidin I) #status experimental <BDY> F:417-488/Region: glycine/histidine/lysine-rich F:19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen F:87-168, 169, 204/Binding site: carbohydrate (Asn) (covalent) #status experimental F:116/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental F:117/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental F:378-389/Cleavage site: Met-Lys (kallikrein) #status experimental F:388-389/Modified site: 4-hydroxyproline (Pro) #status predicted F:398-406, 512/Binding site: carbohydrate (Ser) (covalent) #status experimental F:438-499/Cleavage site: Arg-Thr (kallikrein) #status experimental	
Qy 64 GKKFIDFVARETTCSKSNEELTESCTEKLQGSLDNNAEVVPPWERKTYPTV 118 Db 313 GLKYSIVVFARETTCSKSNEELTKSCSCEINHQILCDANVVVPWEEKVYPTV 367	
RESULT 6	
KGBD12 kininogen, HMW II precursor - bovine N:Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen N:Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen C:Species: Bos primigenius taurus (cattle) C:Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 C:Accession: A01282; A91933; A91938; B29559	
R:Kitamura, N.; Takasaki, Y.; Furuto, S.; Tanaka, T.; Nawa, H.; Nakanishi, S. Nature 305, 545-549, 1983 A:Reference number: A93311; MUID:8014106; PMID:6571699	
Qy 4 KDFVQPKTKIVGCPKPRDIPNSPEELTHTKLNAAENNATYFKIDNVKARQVWV 118 Db 253 KDFVQPKTRICAGCPKRPVPPDLEPLSHSIARKNABHDGAFYFKDTVKATVQVVA 312	

J. Biochem. 67, 313-323, 1970
 A; Title: Studies on the structure of bovine kininogen: cleavages of disulfide bonds and
 A; Reference number: A91923; MUID:70180420; PMID:4986612

A; Molecule type: protein
 A; Residues: 376-391 <KAT>
 R; Han, Y.N.; Kato, H.; Iwanaga, S.; Suzuki, T.
 J. Biochem. 79, 1201-1222, 1976
 A; Title: Primary structure of bovine plasma high-molecular-weight kininogen. The amino acid sequence number: A91938; MUID:5170365; PMID:1169337

A; Accession: A91941
 A; Molecule type: protein
 A; Residues: 387-455 <HAN>
 R; Sueyoshi, T.; Miyata, T.; Hashimoto, N.; Kato, H.; Hayashida, H.; Miyata, T.; Iwanaga, S.; Biol. Chem. 262, 2768-2779, 1987
 A; Title: Bovine high molecular weight kininogen. The amino acid sequence, positions of cysteines and disulfide bonds. Amino acid sequence number: A92627; MUID:3546295

A; Accession: B29559
 A; Molecule type: protein
 A; Residues: 'Z', 20-104, 'B', 106-256, 'XX', 257-376 <SUB>
 R; Loeffelholz, F.; Kellermann, J.; Henschen, A.; Foerstach, B.; Muller-Esterl, W.
 Eur. J. Biochem. 152, 307-314, 1985
 A; Title: The amino acid sequence of the light chain of human high-molecular-mass kininogen
 A; Reference number: A91153; MUID:86030270; PMID:4054110
 A; Contents: annotation; bovine cleavage sites; bovine carbohydrate binding sites
 R; Sueyoshi, T.; Miyata, T.; Kato, H.; Iwanaga, S.
 Seikagaku 56, 808, 1984
 A; Title: Disulfide bonds in bovine HMW kininogens.
 A; Contents: annotation; disulfide bonds
 A; Note: article in Japanese
 C; Comment: Kininogen is produced from the same gene as the LMW form as a cysteine protease inhibitor, takes part in initiation of the HMW kininogen light chain is important for the release of kallikrein, released from kininogen prior to the release of bradykinin.
 C; Comment: The glycine/histidine/lysine-rich region of HMW kininogen light chain is important for the release of bradykinin.
 C; Superfamily: kininogen; cystatin homology
 C; Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; duplication; signal sequence
 F; 19-619/Product: HMW kininogen II #status predicted <SIG>
 F; 19-3/6/Product: HMW kininogen II heavy chain #status experimental <HCH>
 F; 19-130/Domain: cystatin homology <CY1>
 F; 141-252/Domain: cystatin homology <CY2>
 F; 131-372/Domain: cystatin homology <CY3>
 F; 377-386/Product: tyrosyl-bradykinin (kallidin II) #status experimental <KBDY>
 F; 378-386/Product: bradykinin (kallidin I) #status experimental <BDY>
 F; 287-619/Product: HMW kininogen II light chain #status experimental <LCH>
 F; 418-488/Region: glycine/histidine/lysine-rich (Gln) (in mature form) #status experimental
 F; 19-Modified site: pyrrolidine carboxylic acid (Gln) (in mature form) #status experimental
 F; 27-589, 82-93, 106-125, 141-144, 205-217, 228-247, 261-264, 322-337, 348-367/Disulfide bonds:
 F; 47/Binding site: carbohydrate (Asn) (covalent) #status absent
 F; 136/Binding site: carbohydrate (Thr) (covalent) #status experimental
 F; 87-168, 169, 204-280/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
 F; 19/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
 F; 376-377/Cleavage site: Met-Lys (kallikrein) #status predicted
 F; 386-387/Cleavage site: Arg-Ser (kallikrein) #status predicted
 F; 396-400, 404, 510/Binding site: carbohydrate (Ser) (covalent) #status experimental
 F; 397-398, 518, 522-534, 546, 551, 568/Binding site: carbohydrate (Thr) (covalent) #status experimental
 Query Match Score 413; DB 1; Length 619;
 Best Local Similarity 60.1%; Pred. No. 8.2e-31; Indels 2; Gaps 1;

Qy 3 GKDFVQQPTKICVGCPDIPNTSPELEETLTITKLNAAENNATYFKIDNVKKARVQVV 62
 Db 252 GEDFF--PPMVCVGCKPKIPDSDPDEEALNHSIAKLNAHDGTFPKIDTVKKARVQVV 309

Qy 63 AGKRYFIDFVARETTCSKESNEELTSCTKLGQSOLDCNAEVYVTPWEKKIYPTV 118
 Db 310 GSILKYSIVFIARETTCSKGSMNEELTSCE=NIHGQQLHCDANVYTVPWEKKIYPTV 365

RESULT 7
 A; Accession: A28055
 A; Species: Rattus norvegicus (Norway rat)
 C; Sequence: 20-Jun-1989 #sequence_revision 20-Jun-1989 #text_change 15-Nov-1996
 C; Accession: A28055
 C; Superfamily: kininogen; cystatin homology
 C; Keywords: alternative splicing
 F; 1-18/Domain: signal sequence #status predicted <SIG>
 F; 19-433/Domain: K-kininogen, LMW I #status predicted <MAT>
 F; 19-131/Domain: cystatin homology <CY1>
 F; 142-253/Domain: cystatin homology <CY2>
 F; 264-375/Domain: cystatin homology <CY3>
 Query Match Score 59.7%; DB 2; Length 433;
 Best Local Similarity 66.4%; Pred. No. 1.1e-30;
 Matches 77; Conservative 13; Mismatches 26; Indels 0; Gaps 0;

Qy 3 GKDFVQQPTKICVGCPDIPNTSPELEETLTITKLNAAENNATYFKIDNVKKARVQVV 62
 Db 253 GDDLFELLPEDCGCPRNIPVDSPKEALGHISIAQNLAAENHTFYKIDTVKKARVQVV 312

Qy 63 AGKRYFIDFVARETTCSKESNEELTSCTKLGQSOLDCNAEVYVTPWEKKIYPTV 118
 Db 313 AGTXYVIFIARETTCSKESNEELTSCTKLGQSOLNCRANVYMPWENKVPTV 368

RESULT 8
 A; Accession: A25486
 A; Species: Rattus norvegicus (Norway rat)
 C; Sequence: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 15-Nov-1996
 C; Date: 08-Mar-1989 #sequence_revision
 C; Superfamily: kininogen; cystatin homology
 R; Kitagawa, H.; Kitanishi, S.
 J. Biol. Chem. 262, 2190-2198, 1987
 A; Title: Differing expression patterns and evolution of the rat kininogen gene family.
 A; Reference number: A92625; MUID:8713443; PMID:3029068

A; Accession: A25486
 A; Molecule type: mRNA
 A; Residues: 1-639 <KIT>
 A; Note: the authors translated the codon CAA for residue 347 as Asn
 C; Superfamily: kininogen; cystatin homology
 C; Keywords: alternative splicing
 F; 1-18/Domain: signal sequence #status predicted <SIG>
 F; 19-639/Domain: kininogen, HMW I #status predicted <MAT>
 F; 19-131/Domain: cystatin homology <CY1>
 F; 142-253/Domain: cystatin homology <CY2>
 F; 264-375/Domain: cystatin homology <CY3>
 Query Match Score 53.7%; DB 2; Length 639;
 Best Local Similarity 66.4%; Pred. No. 1.6e-30;
 Matches 77; Conservative 13; Mismatches 26; Indels 0; Gaps 0;

Qy 3 GKDFVQQPTKICVGCPDIPNTSPELEETLTITKLNAAENNATYFKIDNVKKARVQVV 62
 Db 314 GSILKYSIVFIARETTCSKGSMNEELTSCE=NIHGQQLHCDANVYTVPWEKKIYPTV 365

RESULT 9

A22897 AGKXYFIDFVARETCSKESNEELTESCTKLQGQLDCAEYVYPWEKKIYPTV 118
 Db 63 QY C;Species: Rattus norvegicus (Norway rat)
 Db 313 AGTKYVIEETARETKCSEKSNABETADCTKLQGSLNCNANVYMRPWEKKVPTV 368
 F:19-130/Domain: cystatin homology <CY2>
 F:19-130/Domain: cystatin homology <CY2>
 F:19-130/Domain: cystatin homology <CY2>

Query Match 56.5%; Score 388; DB 2; Length 430;
 Best Local Similarity 62.1%; Pred. No. 1.2e-28;
 Matches 72; Conservative 15; Mismatches 29; Indels 0; Gaps 0;

Db 3 QY GKDVFQPPFKICVCPDRDIPNTSPELEETLTTKINAENNATYFKIDNVTKKARVQVV 62
 Db 252 QDDLFSLPLPKCGPKNPVDPELKGIAQHHLFVKIDTVKATSQVV 311

QY 63 AGKXYFIDFVARETCSKESNEELTESCTKLQGQLDCAEYVYPWEKKIYPTV 118
 Db 312 AGTKYVIEETARETKCSEKSNABETADCTKLQGSLNCNANVYMRPWEKKVPTV 367

RESULT 11

KGRTM
 A;Molecule type: protein
 A;Accession: A22897
 A;Residues: 1-14 <AND1>
 A;Accession: B23897
 A;Molecule type: mRNA
 A;Residues: 5-430 <AND2>
 A;Cross-references: GB:MI1661; NID:9205307; PIDN:AAA41570.1; PMID:9205308
 A;Note: the authors translated the codon CTC for residue 410 as Arg, CTA for residue 415
 F:19-130/Domain: cystatin homology <CY2>
 F:19-130/Domain: cystatin homology <CY2>
 F:263-374/Domain: cystatin homology <CY3>

Query Match 56.5%; Score 388; DB 2; Length 430;
 Best Local Similarity 62.1%; Pred. No. 1.2e-28;
 Matches 72; Conservative 15; Mismatches 29; Indels 0; Gaps 0;

Db 3 QY GKDVFQPPFKICVCPDRDIPNTSPELEETLTTKINAENNATYFKIDNVTKKARVQVV 62
 Db 252 QDDLFSLPLPKCGPKNPVDPELKGIAQHHLFVKIDTVKATSQVV 311

QY 63 AGKXYFIDFVARETCSKESNEELTESCTKLQGQLDCAEYVYPWEKKIYPTV 118
 Db 312 AGTKYVIEETARETKCSEKSNABETADCTKLQGSLNCNANVYMRPWEKKVPTV 367

RESULT 10

B28055 T-kininogen, LMW II precursor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Accession: B28055; E25466; B28526; C25526
 R;Furuto-Kato, S.; Matsumoto, A.; Kitamura, N.; Nakanishi, S.
 J. Biol. Chem. 260, 12054-12059, 1985
 A;Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin and inhibitor.
 A;Reference number: A92496; MUID:86008264; PMID:2413018
 A;Accession: B22055
 A;Molecule type: mRNA
 A;Residues: 1-430 <FOR>
 R;Kitagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.
 J. Biol. Chem. 263, 973-979, 1988
 A;Title: Purification and characterization of rat T-kininogens isolated from plasma of a
 A;Reference number: A92722; MUID:38087226; PMID:3121673
 A;Accession: B28526
 A;Molecule type: protein
 A;Residues: 'E', 20-25, 'MD', 28-48, 376-430 <ENJ>
 A;Accession: C28526
 A;Molecule type: protein

QY 63 AGKXYFIDFVARETCSKESNEELTESCTKLQGQLDCAEYVYPWEKKIYPTV 118
 Db 305 QY AGTKYVIEETARETKCSEKSNABETADCTKLQGSLNCNANVYMRPWEKKVPTV 360

RESULT 12

KGRTTI
 T-kininogen I precursor - rat
 N;Alternative names: 73K protein; LMW kininogen T-1
 N;Contains: bradykinin; T-kinin
 C;Species: Rattus norvegicus (Norway rat)
 C;Accession: A01286; D25486; A28526; P0193; JQ0027
 C;Accession: A01286; D25486; A28526; P0193; JQ0027; B25485; S68036

R; Furuto-Kato, S.; Matsumoto, A.; Kitamura, N.; Nakaniishi, S.
 J. Biol. Chem. 260, 1254-1259, 1985
 A; Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin and inhibitor.
 A; Reference number: A92496; PMID:86008264; PMID:2413018
 A; Accession: A01286
 A; Molecule type: mRNA
 A; Residues: 1-430 <FR>
 A; Cross-references: GB:MM11883; NID:9205084; PID:AAA1489.1; PID:g205085
 R; Kitamura, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakaniishi, S.
 J. Biol. Chem. 262, 2190-2195, 1987
 A; Title: Differing expression patterns and evolution of the rat kininogen gene family.
 A; Reference number: A92625; MUID:87137443; PMID:3029068
 A; Accession: D25486
 A; Molecule type: DNA
 A; Residues: 375-430 <KIT>
 R; Enyoji, K.; Kato, H.; Hayashi, I.; Ohishi, S.; Iwanaga, S.
 J. Biol. Chem. 263, 973-979, 1988
 A; Title: Purification and characterization of rat T-kininogens isolated from plasma of a
 A; Reference number: A92299; MUID:88087226; PMID:3121623
 A; Accession: A28526
 A; Molecule type: protein
 A; Residues: 'E', 20-48; '376-430 <ENK>
 R; Kanda, S.; Sugiyama, K.; Takahashi, M.; Shumiya, S.; Tomino, S.; Nagase, S.
 Jpn. J. Cancer Res. 81, 63-68, 1990
 A; Title: Identification of a proenzyme increasing in serum of Nagase analbuminemic rats by
 A; Reference number: PL0193; MUID:90216390; PMID:2108848
 A; Molecule type: mRNA
 A; Residues: 330-420, 'R', 422-429, 'P', <KAN>
 R; Anderson, K.P.; Croyle, M.L.; Lingrel, J.B.
 Gene 81, 119-128, 1989
 A; Title: Primary structure of a gene encoding rat T-kininogen.
 A; Reference number: JQ0027; MUID:9034172; PMID:2806508
 A; Accession: JQ0027
 A; Molecule type: DNA
 A; Residues: 1-60, 'E', 62-113, 'R', 115-165, 'F', 167-178, 'TKI', 182-211, 'F', 213-256, 'S', 258-38
 A; Experimental source: strain Sprague-Dawley
 R; Kageyama, R.; Kitamura, N.; Ohkubo, H.; Nakaniishi, S.
 J. Biol. Chem. 262, 2345-2351, 1987
 A; Title: Differing utilization of homologous transcription initiation sites of rat K and
 A; Reference number: A25488; MUID:87137465; PMID:3818398
 A; Accession: B25488
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-48 <RGK>
 A; Cross-references: GB:MM14356; NID:9205090; PID:AAA1492.1; PID:g205091
 R; Enyoji, K.; Kato, H.; Hayashi, I.; Ohishi, S.; Iwanaga, S.
 J. Biol. Chem. 263, 955-972, 1988
 A; Title: Purification and characterization of two kinds of low molecular weight kininogen
 A; Reference number: A28525; MUID:88087225; PMID:3335530
 A; Accession: A28525
 A; Molecule type: protein
 A; Residues: 376-430 <EN2>
 R; Sierra, F.; Walter, R.; Vautravers, P.; Guiago, Y.
 Arch. Biochem. Biophys. 322, 333-338, 1995
 A; Title: Identification of several isoforms of T-kininogen expressed in the liver of agouti
 A; Reference number: S68034; MUID:96032652; PMID:7574705
 A; Accession: S68036
 A; Molecule type: mRNA
 A; Residues: 340-430 <SIE>
 A; Experimental source: clone pSG17
 C; Comment: At least three types of LMW kininogen precursors are present in rat plasma, coding bradykinin.
 C; Comment: T-kininogens contain T-kinin (I-S-bradykinin), a novel kinin isolated after
 d of an Arg or Lys, it is probably not released from its precursor by either tissue or plasma.
 C; Comment: The T-kininogens are produced in response to an inflammatory stimulant.
 C; Genetics: 65/3, 102/3; 130/1; 187/3; 223/2; 252/1; 309/3; 345/3; 374/3; 398/3
 A; Cross-references: EMBL:X52255; NID:CAA36497.1; PID:9296643
 R; Abrahamsson, M.; Olatsson, I.; Grubb, A.; Olafsson, I.; Lundwall, A.
 FEBS Lett. 216, 229-233, 1990
 A; Title: Molecular cloning and sequence analysis of cDNA coding for the precursor of the
 A; Reference number: S00004; MUID:87219149; PMID:3495457

F; 19-130/Domain: cystatin homology <CY1>
 F; 141-252/Domain: cystatin homology <CY2>
 F; 263-374/Domain: cystatin homology <CY3>
 F; 378-386/Product: bradykinin #status Predicted <BDY>
 F; 19/Mod/Fld site: Pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment
 F; 82-126, 168, 204, 326/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F; 83-94, 107-125, 141-144, 205-217, 228-247, 263-266, 327-339, 350-369/Disulfide bonds: #status
 Query Match Score 380; DB 1; Length 430;
 Best Local Similarity 62.1%; Pred. No. 6.7e-28;
 Matches 14; Mismatches 30; Indels 0; Gaps 0;
 Qy 3 GRDFVQEPKICVGCRDIPNTSPEBEITLTTIKLNAAENATFKIDNKKARVQVV 62
 Db 252 GDDLFELLPKRNCRGCRCREIPDSPEIKEALGHSTACLNACHNHFVKIDTVKRSQSQQV 311
 Qy 63 AGKKYFIDEVARETTCSKESNEELTSCETKLKGQSLDCNAEVVTPWPWERKIPTV 118
 Db 312 ACVIVVIEIFIARETNCSKQSKTLETAADCETKHLGQSLNCNAVNMPWENKVVPY 367
 RESULT 13
 UDB0
 cystatin - bovine
 N; Alternative names: thiol proteinase inhibitor
 C; Species: Bos primigenius taurus (cattle)
 C; Date: 28-Feb-1986 #sequence_change 06-Dec-1996
 C; Accession: A01271
 R; Hirado, M.; Tsunabawa, S.; Sakiyama, F.; Fujiose, M.; Fujii, S.
 FEBS Lett. 186, 41-45, 1985
 A; Title: Complete amino acid sequence of bovine colostrum low-M-r cysteine proteinase inhibitor
 A; Reference number: A01271; MUID:85231205; PMID:3891407
 A; Accession: A01271
 A; Molecule type: protein
 A; Residues: 1-112 <HR>
 C; Superfamily: cystatin; cystatin homology
 C; Keywords: colostrum; cysteine protease inhibitor
 F; 2-112/Domain: cystatin homology <CYS>
 F; 48-52/Region: inhibitory #status predicted
 F; 66-76, 90-110/Disulfide bonds: #status predicted
 Query Match Score 20.0%; DB 1; Length 112;
 Best Local Similarity 28.8%; Pred. No. 7.5e-06;
 Matches 32; Conservative 25; Mismatches 35; Indels 19; Gaps 4;
 Qy 24 NSPBLEETLTTIKLNAAENATFKIDNKKARVQVVAKYFDFVARETTCSKESN 83
 Db 12 NEEGVQEAISPAVSEFNKRSNDAYQSRVVRVTRARKQVSVGMNFYDVELGRTCTK-S 69
 Qy 84 EELTECS-----ETKLKGQSLDCNAEVVTPWPWERKIPTVNEWECE 126
 Db 70 QANLSDCPFHNDQHLLKREKL-----CSFQVTVPPWN-----TINLVKFSCQ 111
 RESULT 14
 UDPH
 cystatin C precursor [validated] - human
 N; Alternative names: Gamma-CSF; gamma-trace; neuroendocrine basic polypeptide; post-gamma i
 C; Species: Homo sapiens (man)
 C; Date: 06-Jul-1982 #sequence_revision 31-Mar-1991 #text_change 08-Dec-2000
 C; Accession: S10216/S00004; JLU095; A32751; A01270; A25444; S12288; A32732; A600
 R; Abrahamsson, M.; Olatsson, I.; Palsdottir, A.; Urvsbaek, M.; Lundwall, A.; Jansson, O.
 Biochem. J. 268, 287-294, 1990
 A; Title: Structure and expression of the human cystatin C gene.
 A; Reference number: S10216; MUID:90303202; PMID:2363674
 A; Molecule type: DNA
 A; Residues: 1-146 <AB1>
 A; Cross-references: EMBL:X52255; NID:CAA36497.1; PID:9296643
 R; Abrahamsson, M.; Grubb, A.; Olafsson, I.; Lundwall, A.
 FEBS Lett. 216, 229-233, 1990
 A; Title: Molecular cloning and sequence analysis of cDNA coding for the precursor of the
 A; Reference number: S00004; MUID:87219149; PMID:3495457

A;Accession: S00004
A;Molecule type: mRNA
A;Residues: 1-146 <AB2>
A;Cross references: EMBL:X05607; PIDN:CAA29096.1; PMID:9755738
R; Levy, B.; Lopez-Otin, C.; Ghiso, J.; Geltner, D.; Frangione, B.
J. Exp. Med. 169, 1771-1778, 1989
A;Title: Stroke in Icelandic patients with hereditary amyloid angiopathy is related to a
A;Reference number: JU0095; MUID:89235594; PMID:25411223
A;Accession: JU0095
A;Molecule type: DNA
A;Residues: 1-146 <LEN>
A;Cross references: GB:X61681; NID:930371; PIDN:CAA43086.2; PIDN:94490344
A;Note: the cystatin C gene isolated from the brain of an Icelandic patient with heredit
e)
R; Saitoh, E.; Sabatini, L.M.; Eddy, R.L.; Shows, T.B.; Azen, E.A.; Iseura, S.; Satada,
Biochem. Biophys. Res. Commun. 162, 1324-1331, 1989
A;Title: The human cystatin C gene (CST3) is a member of the cystatin gene family which
A;Reference number: A33400; MUID:89350949; PMID:2764935
A;Accession: A33400
A;Molecule type: DNA
A;Residues: 1-24 /'T', 26-146 <SAI>
A;Cross references: GB:M27889; GB:M27890; GB:M27891; NID:9181385; PIDN:AAA52164.1; PMID:9
A;Title: Isolation of a sequence encoding human cystatin C. Conservation of exon-intron
A;Reference number: S02751; MUID:89076507; PMID:3264504
A;Accession: S02751
A;Molecule type: DNA
A;Cross references: EMBL:M27769
A;Residues: 8-119 <GH2>
R; Ghiso, J.; Jenson, O.; Frangione, B.
Proc. Natl. Acad. Sci. U.S.A. 79, 3024-3027, 1982
A;Title: Human gamma-trace, a basic microprotein: amino acid sequence and presence in th
A;Reference number: A01270; MUID:8222268; PMID:6283552
A;Accession: A01270
A;Molecule type: protein
A;Residues: 27-131 /'S', 133-146 <GRU>
R; Grubb, A.; Lofberg, H.
Proc. Natl. Acad. Sci. U.S.A. 83, 2974-2978, 1986
A;Title: Amyloid fibrils in hereditary cerebrovascular hemorrhage with amyloidosis of Iceland
A;Reference number: A25434; MUID:86206076; PMID:517880
A;Accession: A25434
A;Molecule type: protein
A;Residues: 37-93, Q /'95-146 <GH1>
R; Turk, V.; Brzin, J.; Longer, M.; Ritonja, A.; Brodin, M.; Borchart, U.; Machleidt, W.
Hoppe-Seyler's Z. Physiol. Chem. 364, 1487-1496, 1983
A;Title: Protein inhibitors of cysteine proteases. III. Amino-acid sequence of cystati
A;Reference number: S01461; MUID:8410059; PMID:6662498
A;Accession: S12288
A;Molecule type: protein
R; Brzin, J.; Popovic, T.; Turk, V.
Biochem. Biophys. Res. Commun. 118, 103-109, 1984
A;Title: Human Cystatin, a new protein inhibitor of cysteine proteinases.
A;Reference number: A32732; MUID:84128015; PMID:6365034
A;Accession: A32732
A;Molecule type: protein
A;Residues: 27-76 <BRZ>
R; Olaisson, I.; Gudmundsson, G.; Abrahamsson, M.; Jansson, O.; Grubb, A.
Scand. J. Clin. Lab. Invest. 50, 85-93, 1990
A;Title: The amino terminal portion of cerebrospinal fluid cystatin C in hereditary cyst
A;Reference number: A60552; MUID:90193615; PMID:2315617
A;Accession: A60552
A;Molecule type: protein
A;Residues: 27-49, XX, 52-64 <OLA>
A;Note: this protein is purified from cerebrospinal fluid of patients with the autosomal d
e defective gene is not present in CSF but is found instead in amyloid deposits
R; Popovic, T.; Brzin, J.; Ritonja, A.; Turk, V.
Biochem. Hoppe-Seyler 371, 575-580, 1990
A;Title: Different forms of human cystatin C.
A;Reference number: S10607; MUID:31025625; PMID:2222856
A;Accession: S10607

A;Molecule type: protein
A;Residues: 27-53 <POP>
A;Experimental source: urine, kidney disease
A;Note: truncated forms with amino ends at positions 35 and 36 of the precursor were also
R; Grubb, A.; Lofberg, H.; Barrett, A.J.
FEBS Lett. 170, 370-374, 1984
A;Title: The disulfide bridges of human cystatin C (gamma-trace) and chicken cystatin.
A;Reference number: S0462
A;Contents: annotation, disulfide bonds
R; Bertti, P.J.; Storer, A.C.
Biochem. J. 302, 411-416, 1994
A;Title: Local pH-dependent conformational changes leading to proteolytic susceptibility
A;Reference number: S553305; MUID:8032991
A;Accession: 955305
A;Molecule type: protein
A;Residues: 27-49/106-146 <BER>
C;Comment: This protein is found in the post-globulin fraction of cerebrospinal fluid
f patients with certain autoimmune diseases.
C;Comment: This protein is an inhibitor of cysteine proteinases and may serve an important
C;Genetics:
A;Gene: GDB:CST3
A;Cross References: GDB:119817; OMIM:105150
A;Map position: 20p11.2-20p11.2
A;Introns: 81/3; 119/3
C;Keywords: amyloid; cysteine proteinase inhibitor; extracellular protein; hydroxyproline
C;Superfamily: cystatin homology
F:1-26/Domain: cystatin homology <CR>
F:55-146/Domain: cystatin homology <CR>
F:81-85/Region: inhibitory #status predicted
F:23/Modifield site: hydroxyproline (Pro) (partial) #status experimental
F:39-109,123-143/Disulfide bonds: #status experimental

Query Match Score 132.5: Best Local Similarity 27.0%; Pred. No. 2.9e-05;
Matches 33; Conservation 25; Mismatches 53; Indels 11; Gaps 4;

QY 8 QPPTKICVGCPDIPTNSPEELTITHITKINAENNATEYFKIDNKVKARQVYAGKVKY 67
Db 31 KPPR--LVGGMDASVSEEGVRALDFAVGYNKAANDMTYSRALQVYRKQIVAGVNY 88

QY 68 FIDFVAEETTCSESNEELTESC--ETKKLGQSLLDNCAEVYVWEEKKTPYTWNHE 124
Db 89 FIDFVELGRTCTIC--TQPNLDNCFPHDQPHLKRAFCSFQIYAVPWQ---GTMILSKST 142

QY 125 CE 126
Db 143 CQ 144

RESULT 15
S07085
Cystatin C precursor - rat (Fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 01-Dec-1993 #sequence revision 03-Aug-1995 #text_change 16-Jul-1999
C;Accession: S07085
C;Sequence: S01337; S21109
R; Cole, T.; Dickson, P.W.; Esnard, F.; Averill, S.; Risbridger, G.P.; Gauthier, F.; Schre
R; J. Biochem. 186, 35-42, 1989
A;Title: The cDNA structure and expression analysis of the genes for the cysteine protein
A;Reference number: S07085; MUID:90092122; PMID:2689174
A;Accession: S07085
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 1-172 <COL>
A;Cross-references: EMBL:X16957; PIDN:CAA34831.1; PMID:9736290
R; Esnard, A.; Baudard, F.; Faucher, D.; Gauthier, F.
FEBS Lett. 236, 475-478, 1988
A;Title: Two rat homologues of human cystatin C.
A;Reference number: S01337; MUID:88313020; PMID:3044831
A;Accession: S01337
A;Molecule type: protein

A;Residues: 8-49 <ESN>
R;Esnard, A.; Esnard, F.; Guillou, F.; Gauthier, F.
P;EBS Lett. 300, 131-135 1992
A;Title: Production of the cysteine proteinase inhibitor cystatin C by rat Sertoli cells
A;Reference number: S21109; PMID:1563513
A;Accession: S21109
A;Molecule type: protein
A;Residues: 8, XX, 11-20 <ES2>
C;Superfamily: cystatin; cystatin homology
C;Keywords: cystatin proteinase inhibitor
F;16-127/Domain: cystatin homology <CYS>
F;80-90,104-124/Disulfide bonds: #status predicted

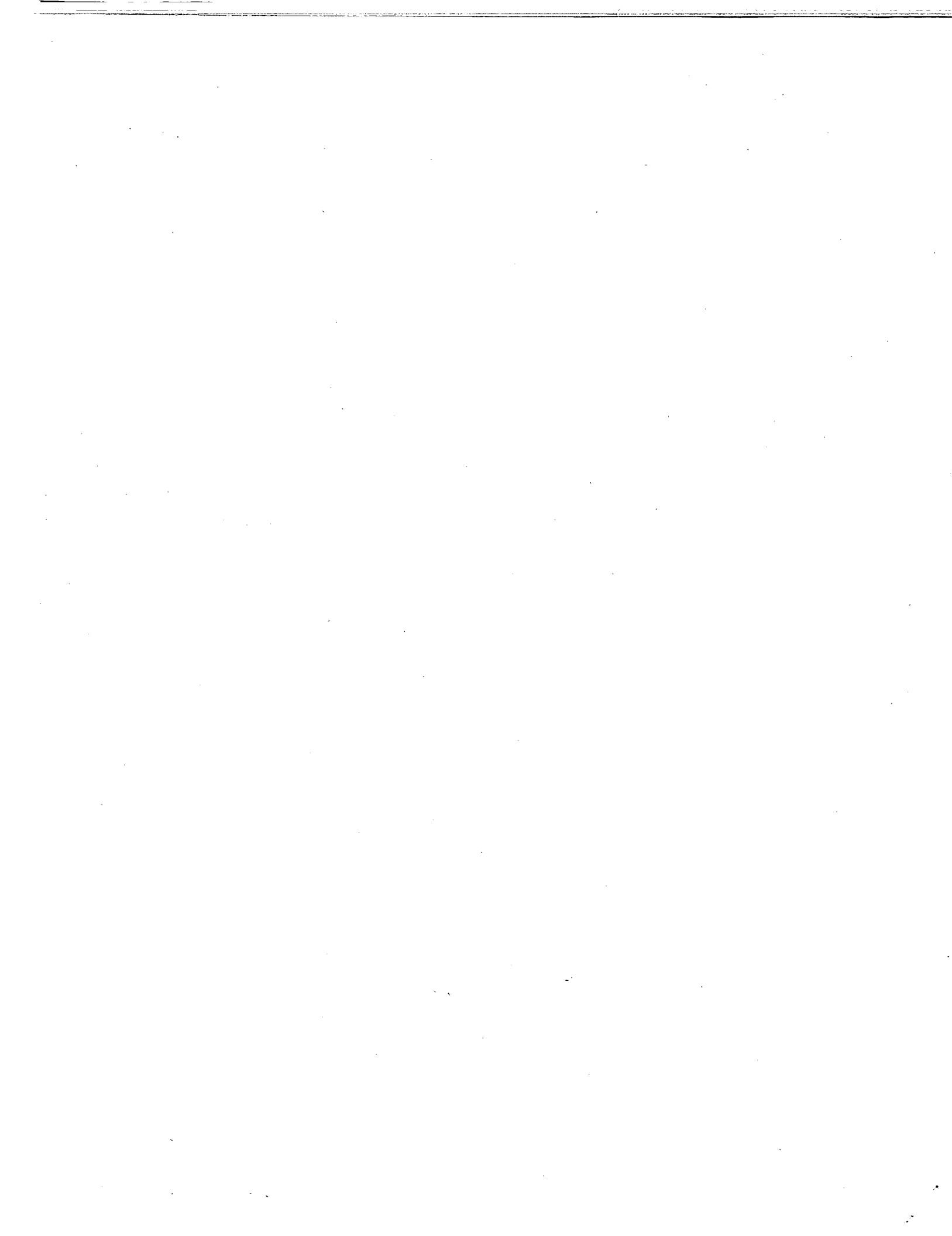
Query Match 18.9%; Score 130; DB 2; Length 127;
Best Local Similarity 28.0%; Pred. No. 4.3e-05;
Matches 30; Conservative 28; Nsmatches 43; Indels 6; Gaps 4;

QY 8 QPPTKICVGCPRDIPNSPELEETLHTTKLNENNATPFKIDDNVKARVQVAGKRY 67
Db 11 RPPPRI-LGAPQEADASEGVQLRADFAUSEYNKGSDNDAYHSRAIQVYFARKQLVAGINY 69

QY 68 FIDFVARETCCKSKESEELTESC---ETKLKGQSLDCNAEVYYFWE 111

Db 70 YLDVENGRTCTK-SQTNLT-NCPPHDQPHLMRKALCSQIYSVFWK 114

Search completed: September 24, 2004, 14:10:49
Job time : 14.716 secs



; PRIOR APPLICATION NUMBER: 60/296,404
 ; PRIOR FILING DATE: 2001-06-06
 ; PRIOR APPLICATION NUMBER: 60/296,418
 ; PRIOR FILING DATE: 2001-06-06
 ; PRIOR APPLICATION NUMBER: 60/297,414
 ; PRIOR FILING DATE: 2001-06-11
 ; PRIOR APPLICATION NUMBER: 60/297,567
 ; PRIOR FILING DATE: 2001-06-12
 ; PRIOR APPLICATION NUMBER: 60/298,285
 ; PRIOR FILING DATE: 2001-06-14
 ; PRIOR APPLICATION NUMBER: 60/298,556
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/299,949
 ; PRIOR FILING DATE: 2001-06-21
 ; PRIOR APPLICATION NUMBER: 60/300,883
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; SEQ ID NO: 82
 ; LENGTH: 390
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-162-335-82

Query Match 90.0%; Score 618; DB 15; Length 390;
 Best Local Similarity 100.0%; Pred. No. 5.7e-59; Indels 0; Gaps 0;
 Matches 116; Conservative 0; Mismatches 0; Gaps 0;

Qy	3	GKDFVQPTKICVGCPDIPNTSPELEETLTITKLNAENNATYFKIDNVKARVQVV	62
Db	216	GKDFVQPTKICVGCPDIPNTSPELEETLTITKLNAENNATYFKIDNVKARVQVV	275
Qy	63	AGKKYFIDFVARETTCSKESNEELTSCETKLGQSOLDCNAAEVYVWPWEEKIYPTV	118
Db	276	AGKKYFIDFVARETTCSKESNEELTSCETKLGQSOLDCNAAEVYVWPWEEKIYPTV	331

Remaining Prior Application data removed - See File Wrapper or PALM.
 ; SEQ ID NO: 201
 ; LENGTH: 398
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-162-335-70

Query Match 90.0%; Score 618; DB 15; Length 398;
 Best Local Similarity 100.0%; Pred. No. 5.8e-59; Indels 0; Gaps 0;
 Matches 116; Conservative 0; Mismatches 0; Gaps 0;

Qy	3	GKDFVQPTKICVGCPDIPNTSPELEETLTITKLNAENNATYFKIDNVKARVQVV	62
Db	224	GKDFVQPTKICVGCPDIPNTSPELEETLTITKLNAENNATYFKIDNVKARVQVV	283
Qy	63	AGKKYFIDFVARETTCSKESNEELTSCETKLGQSOLDCNAAEVYVWPWEEKIYPTV	118
Db	284	AGKKYFIDFVARETTCSKESNEELTSCETKLGQSOLDCNAAEVYVWPWEEKIYPTV	339

RESULT 2
 US-10-162-335-70

Sequence 70, Application US/10162335
 ; Publication No. US20040009480A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, David W.
 ; APPLICANT: Baumgartner, Jason C.
 ; APPLICANT: Boldog, Ferenc I.
 ; APPLICANT: Casman, Stacie J.
 ; APPLICANT: Edinger, Salomit R.
 ; APPLICANT: Gangolli, Esha A.
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Gorman, Linda
 ; APPLICANT: Guo, Xiaojia (Sasha)
 ; APPLICANT: Hjalt, Torod
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Li, Li
 ; APPLICANT: MacDougall, John R.
 ; APPLICANT: Malivankar, Uriel M.
 ; APPLICANT: Millee, Isabelle
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Parturajan, Meera
 ; APPLICANT: Pena, Carol E. A.
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: Stone, David J.
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: Verner, Corine A. M.
 ; APPLICANT: Voss, Edward Z.
 ; APPLICANT: Zethusen, Bryan D.
 ; TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method
 ; CURRENT APPLICATION NUMBER: US7/10/162,335
 ; CURRENT FILING DATE: 2002-10-01
 ; PRIOR APPLICATION NUMBER: 60/295,607
 ; PRIOR FILING DATE: 2001-06-04

; SEQ ID NO: 29
 ; LENGTH: 427;
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incyte ID No. US20030108871A1 167507CD1
 US-09-919-039-29

Query Match 90.0%; Score 618; DB 10; Length 427;
 Best Local Similarity 100.0%; Pred. No. 6.4e-59; Indels 0; Gaps 0;
 Matches 116; Conservative 0; Mismatches 0; Gaps 0;

Qy	3	GKDFVQPTKICVGCPDIPNTSPELEETLTITKLNAENNATYFKIDNVKARVQVV	62
Db	253	GKDFVQPTKICVGCPDIPNTSPELEETLTITKLNAENNATYFKIDNVKARVQVV	312
Qy	63	AGKKYFIDFVARETTCSKESNEELTSCETKLGQSOLDCNAAEVYVWPWEEKIYPTV	118
Db	313	AGKKYFIDFVARETTCSKESNEELTSCETKLGQSOLDCNAAEVYVWPWEEKIYPTV	368

RESULT 4
US-10-162-335-72
Sequence 72, Application US/10162335
Publication No. US20040009480A1
GENERAL INFORMATION:
APPLICANT: Anderson, David W.
APPLICANT: Baumgartner, Jason C.
APPLICANT: Boldog, Ferenc L.
APPLICANT: Casman, Shlomit R.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Ganssoll, Esha A.
APPLICANT: Gerlach, Valerie
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Hjalti, Tord
APPLICANT: Kekuda, Ramesh
APPLICANT: Li, Li
APPLICANT: Macdougall, John R.
APPLICANT: Malvankar, Uriel M.
APPLICANT: Millet, Isabelle
APPLICANT: Padigaru, Muralidhara
APPLICANT: Patturajan, Meera
APPLICANT: Pena, Carol E. A.
APPLICANT: Rascelli, Luca
APPLICANT: Shimkets, Richard A.
APPLICANT: Stone, David J.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Vernet, Corine A. M.
APPLICANT: Voss, Edward Z.
TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method
FILE REFERENCE: 21402-377 B
CURRENT APPLICATION NUMBER: US/10/162,335
CURRENT FILING DATE: 2002-10-01
PRIORITY NUMBER: 60/295,607
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/295,661
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/296,404
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/296,418
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/297,414
PRIOR FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 60/297,567
PRIOR FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: 60/298,285
PRIOR FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 60/298,556
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/299,949
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 60/300,883
PRIOR FILING DATE: 2001-06-26
Remaining Prior Application data removed - See File Wrapper or PALM.

SEQ ID NO: 201
LENGTH: 615
TYPE: PRT
ORGANISM: Homo sapiens

US-10-162-335-72
Query Match: 90.0%; Score: 618; DB: 15; Length: 615;

Best Local Similarity: 100.0%; Pred. No. 1e-58; Indels: 0; Gaps: 0;
Matches: 116; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

Oy 3 GRDEVQPTKIKCIVGCPDIPNTNSPELEETLTITKNAENNATPFKIDNVKKARQVY 62

Db 224 GRDFVQPPKIKCIVGCPDIPNTNSPELEETLTITKNAENNATPFKIDNVKKARQVY 283

Oy 63 AGKRYFIDFVARETTCSESNEELTESSCTKLGQSLLDCNAEVTVPPWEKKIYPTV 118

RESULT 5
US-10-162-335-74
Sequence 74, Application US/10162335
Publication No. US20040009480A1
GENERAL INFORMATION:
APPLICANT: Anderson, David W.
APPLICANT: Baumgartner, Jason C.
APPLICANT: Boldog, Ferenc L.
APPLICANT: Casman, Shlomit R.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Gangolli, Esha A.
APPLICANT: Gerlach, Valerie
APPLICANT: Gorman, Linda
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Hjalti, Tord
APPLICANT: Kekuda, Ramesh
APPLICANT: Li, Li
APPLICANT: Macdougall, John R.
APPLICANT: Malvankar, Uriel M.
APPLICANT: Millet, Isabelle
APPLICANT: Padigaru, Muralidhara
APPLICANT: Patturajan, Meera
APPLICANT: Pena, Carol E. A.
APPLICANT: Rascelli, Luca
APPLICANT: Shimkets, Richard A.
APPLICANT: Stone, David J.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Vernet, Corine A. M.
APPLICANT: Voss, Edward Z.
APPLICANT: Zerhusen, Bryan D.
TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method
FILE REFERENCE: 21402-377 B
CURRENT APPLICATION NUMBER: US/10/162,335
CURRENT FILING DATE: 2002-10-01
PRIORITY NUMBER: 60/295,607
PRIOR APPLICATION NUMBER: 60/295,607
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/295,661
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/296,404
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/296,418
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/297,414
PRIOR FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 60/297,567
PRIOR FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: 60/298,285
PRIOR FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 60/298,556
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/299,949
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 60/300,883
PRIOR FILING DATE: 2001-06-26
Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 201
NUMBER OF SEQ ID NOS: 201
SEQ ID NO: 74
LENGTH: 644
TYPE: PRT
ORGANISM: Homo sapiens

US-10-162-335-74
Query Match: 90.0%; Score: 618; DB: 15; Length: 644;

Best Local Similarity: 100.0%; Pred. No. 1.e-58; Indels: 0; Gaps: 0;
Matches: 116; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

Oy 3 GKDFVQPPKIKCIVGCPDIPNTNSPELEETLTITKNAENNATPFKIDNVKKARQVY 62

Db 253 GKDFVQPPKIKCIVGCPDIPNTNSPELEETLTITKNAENNATPFKIDNVKKARQVY 312

Oy 63 AGKRYFIDFVARETTCSESNEELTESSCTKLGQSLLDCNAEVTVPPWEKKIYPTV 118

RESULT 6

Sequence 84, Application US/10162335
Publication No. US2004009480A1
GENERAL INFORMATION:
 ; APPLICANT: Anderson, David W.
 ; APPLICANT: Baumgartner, Jason C.
 ; APPLICANT: Boldog, Ferenc L.
 ; APPLICANT: Casman, Stacie J.
 ; APPLICANT: Edinger, Shlomit R.
 ; APPLICANT: Gangolli, Estha A.
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Gorman, Linda
 ; APPLICANT: Guo, Xiaojia (Sasha)
 ; APPLICANT: Hjalt, Tord
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Li, Li
 ; APPLICANT: MacDougal, John R.
 ; APPLICANT: Millet, Isabelle
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Palyankar, Uriel M.
 ; APPLICANT: Pena, Carol E. A.
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Shimkevits, Richard A.
 ; APPLICANT: Stone, David J.
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: Vernet, Corine A. M.
 ; APPLICANT: Voss, Edward Z.
 ; APPLICANT: Zerhusen, Bryan D.

TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method
 FILE REFERENCE: 21402-377 B

CURRENT APPLICATION NUMBER: US/10/162,335
 CURRENT FILING DATE: 2002-10-01
 PRIOR APPLICATION NUMBER: 60/1295,607
 PRIOR FILING DATE: 2001-06-14
 PRIOR APPLICATION NUMBER: 60/1295,661
 PRIOR FILING DATE: 2001-06-04
 PRIOR APPLICATION NUMBER: 60/1296,404
 PRIOR FILING DATE: 2001-06-06
 PRIOR APPLICATION NUMBER: 60/1296,418
 PRIOR FILING DATE: 2001-06-06
 PRIOR APPLICATION NUMBER: 60/1297,414
 PRIOR FILING DATE: 2001-06-11
 PRIOR APPLICATION NUMBER: 60/1297,567
 PRIOR FILING DATE: 2001-06-12
 PRIOR APPLICATION NUMBER: 60/1298,285
 PRIOR FILING DATE: 2001-06-14
 PRIOR APPLICATION NUMBER: 60/1298,556
 PRIOR FILING DATE: 2001-06-15
 PRIOR APPLICATION NUMBER: 60/1299,949
 PRIOR FILING DATE: 2001-06-21
 PRIOR APPLICATION NUMBER: 60/1300,883
 PRIOR FILING DATE: 2001-06-26

Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 201
 SEQ ID NO: 94
 LENGTH: 644
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-162-35-84

Query Match 90.0%; Score 618; DB 15; Length 644;
 Best Local Similarity 100.0%; Pred. No. 1.e-58;
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 3 GKDFVQPPTRKICVGCPBDIPTNSPELEITHTKLNAAANNATYFKIDNVKKARQVV 62

RESULT 7

US-10-316-253-217

Sequence 217, Application US/10316253
 Publication No. US2003016270A1
 GENERAL INFORMATION:
 ; APPLICANT: The Procter & Gamble Company
 ; APPLICANT: Peters, Kevin
 ; APPLICANT: Thompson, Larry
 ; APPLICANT: Wang, Feng
 ; APPLICANT: Greis, Kenneth
 ; TITLE OF INVENTION: Angiogenesis Modulating Proteins
 ; FILE REFERENCE: 8865M
 ; CURRENT APPLICATION NUMBER: US/10/316,253
 ; CURRENT FILING DATE: 2002-12-10
 ; PRIOR APPLICATION NUMBER: US 60/355,295
 ; PRIOR FILING DATE: 2002-02-08
 ; NUMBER OF SEQ ID NOS: 308
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 217
 ; LENGTH: 424
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 ; US-10-316-253-217

Query Match 55.5%; Score 381; DB 14; Length 424;
 Best Local Similarity 62.1%; Pred. No. 5.e-33;
 Matches 72; Conservative 14; Mismatches 30; Indels 0; Gaps 0;

Query 3 GKDFVQPPTRKICVGCPBDIPTNSPELEITHTKLNAAANNATYFKIDNVKKARQVV 62
 ; SEQ ID NO: 217

RESULT 8

US-10-316-253-215

Sequence 215, Application US/10316253
 Publication No. US2003016270A1
 GENERAL INFORMATION:
 ; APPLICANT: The Procter & Gamble Company
 ; APPLICANT: Peters, Kevin
 ; APPLICANT: Thompson, Larry
 ; APPLICANT: Wang, Feng
 ; APPLICANT: Greis, Kenneth
 ; TITLE OF INVENTION: Angiogenesis Modulating Proteins
 ; FILE REFERENCE: 8865M
 ; CURRENT APPLICATION NUMBER: US/10/316,253
 ; CURRENT FILING DATE: 2002-12-10
 ; PRIOR APPLICATION NUMBER: US 60/355,295
 ; PRIOR FILING DATE: 2002-02-08
 ; NUMBER OF SEQ ID NOS: 308
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 215
 ; LENGTH: 430
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 ; US-10-316-253-215

Query Match 55.3%; Score 380; DB 14; Length 430;
 Best Local Similarity 62.1%; Pred. No. 7.e-33;
 Matches 72; Conservative 14; Mismatches 30; Indels 0; Gaps 0;

Query 3 GKDFVQPPTRKICVGCPBDIPTNSPELEITHTKLNAAANNATYFKIDNVKKARQVV 312

Query Match 63 AGKXYFIDFVARETTCSESNEELTESCETKLQGSLDCNAEYVVPWEKLYPTV 118
 Best Local Similarity 100.0%; Pred. No. 1.e-58;
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 313 AGKXYFIDFVARETTCSESNEELTESCETKLQGSLDCNAEYVVPWEKLYPTV 368

RESULT 9
 US-10-329-428-2
 Sequence 2, Application US/10329428
 Publication No. US2003011464A1
 GENERAL INFORMATION:
 APPLICANT: Li, et al.
 TITLE OF INVENTION: Human Cystatin F
 FILE REFERENCE: PF265P1D2
 CURRENT APPLICATION NUMBER: US/10/329,428
 CURRENT FILING DATE: 2002-12-27
 PRIOR APPLICATION NUMBER: 60/014,795
 PRIOR FILING DATE: 1996-04-03
 PRIOR APPLICATION NUMBER: 08/832,535
 PRIOR FILING DATE: 1997-04-03
 PRIOR APPLICATION NUMBER: 09/019,485
 PRIOR FILING DATE: 1998-01-29
 PRIOR APPLICATION NUMBER: 09/528,436
 PRIOR FILING DATE: 2000-03-17
 NUMBER OF SEQ ID NOS: 16
 SEQ ID NO: 2
 SOFTWARE: Patentin version 3.2
 LENGTH: 145
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-329-428-2

Query Match, 23.8%; Score 163.5; DB 14; Length 145;
 Best Local Similarity 31.6%; Pred. No. 9.7e-10;
 Matches 37; Conservative 22; Mismatches 45; Indels 13; Gaps 3;

RESULT 10
 US-09-746-783-197
 Sequence 197, Application US/09746783
 GENERAL INFORMATION:
 APPLICANT: Jacobs, Kenneth
 ADDRESS: Genetics Institute, Inc.
 STREET: 87 Cambridge Park Drive
 CITY: Cambridge
 STATE: MA
 COUNTRY: U.S.A.
 ZIP: 02140
 COMPUTER READABLE FORM:

TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
 NUMBER OF SEQUENCES: 231
 CORRESPONDENCE ADDRESS: ENCODING THEM
 APPLICANT: Fechner, Kim
 McCoy, John M.
 Lavallie, Edward R.
 Racie, Lisa A.
 Tracy, Maurice
 Spaulding, Vicki
 Agostino, Michael J.
 Howes, Steven H.

APPLICANT: Fechner, Kim
 McCoy, John M.
 Lavallie, Edward R.
 Racie, Lisa A.
 Tracy, Maurice
 Spaulding, Vicki
 Agostino, Michael J.
 Howes, Steven H.
 Fechner, Kim
 McCoy, John M.
 Lavallie, Edward R.
 Racie, Lisa A.
 Tracy, Maurice
 Spaulding, Vicki
 Agostino, Michael J.
 Howes, Steven H.

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0., Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/746,783
 FILING DATE: 21-Dec-2000
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Milasincic, Debra J.
 REGISTRATION INFORMATION:
 REGISTRATION NUMBER: 46,931
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEX/FAX: (617) 742-4214
 INFORMATION FOR SEQ ID NO: 197:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 167 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 197:
 US-09-746-783-197
 Query Match, 23.8%; Score 163.5; DB 10; Length 167;
 Best Local Similarity 31.6%; Pred. No. 1.1e-09;
 Matches 37; Conservative 22; Mismatches 45; Indels 13; Gaps 3;
 Qy 11 TKICVGCPDRIPINSPPELEETLTHITKLNAAENNATFYKIDNVKKARVQVY 62
 Db 54 SRYVPGFPXTKNDPGVQLQAARYSVEKFNNCTNDMFLFESRITALVQIVGLKYM 113
 Qy 71 FVARETTCSKESNEELTESCE--TKKLGOSLDCNAAEVYVVPWEKIKYPTVTWVHWE 124
 Db 114 VEIGRTTCKKQNHRL-DDCDFQTNTLHQTLSCYSEWWVWP-----LQHFE 160
 RESULT 11
 US-09-969-834-1
 Sequence 1, Application US/09969834
 ; Patent No. US20020102711A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sandman, Olga K.
 ; GOI, Surya K.
 ; TITLE OF INVENTION: NOVEL HUMAN CYSTATIN-LIKE
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq For Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/969,834
 ; FILING DATE: 01-Oct-2001
 ; CLASSIFICATION: <Unknown>
 ; APPLICATION NUMBER: US/09/471,765
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: US/08/791,522
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: 09/471,765
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749

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; REFERENCE/DOCKET NUMBER: PF-0193 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: 30443
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-969-834-1

Query Match 23.7%; Score 163; DB 9; Length 178;
Best Local Similarity 34.0%; Pred. No. 1.4e-09;
Matches 35; Conservative 20; Mismatches 44; Indels 4; Gaps 2;
Qy 11 1TKICVGCPRDIPNSPELEETLTHITKLNAAENNATYFKIDNVKKARVQQVAGKRYFID 70
Db 54 SRRVKPGPFKTKTNDPSVLQAARYSTVEKFNNCTNDMFLKESRTRALVQIVKHKYMLE 113
Qy 71 FVARETTCSKENEELTESC--TRKLQGSLDCLNDAEYVVVPW 110
Db 114 VEIGRTICKQNHRL-DDCDQFQTNTHTLQKPLSCTYSEWVTVVPW 155

RESULT 12
US-09-775-932-14
Sequence 14, Application US/09775932
Patent No. US20020137671A1
GENERAL INFORMATION
APPLICANT: University of British Columbia
TITLE OF INVENTION: Production and use of Modified Cystatins
FILE REFERENCE: 58.069
CURRENT APPLICATION NUMBER: US/09/775,932
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: CA99-00717
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 60/095,503
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 121
TYPE: PRT
ORGANISM: Homo sapiens
US-09-775-932-14

Query Match 20.2%; Score 138.5; DB 9; Length 121;
Best Local Similarity 31.5%; Pred. No. 4.2e-07;
Matches 34; Conservative 22; Mismatches 45; Indels 7; Gaps 3;
Qy 10 PTKICVGCPRDIPNSPELEETLTHITKLNAAENNATYFKIDNVKKARVQQVAGKRYFID 69
Db 2 PQERMVGEGLRDLSPDDPQVKAAQAVASYNMGNSNIIYFPDTHIKAQSOLVAGKRYFID 61
Qy 70 DVARRETTCSKE--SNEELTESCETKLQQ--SLDCNAEYVVVPW 111
Db 90 TMENGSTDRCRTRVTDGHVDLT-TCPLAGAQOEKRCDFEVLVVPWQ 115

RESULT 14
US-09-940-497-2
Sequence 2, Application US/09940497
Patent No. US20020032476A1
GENERAL INFORMATION
APPLICANT: Ni et al.
TITLE OF INVENTION: Human Cystatin E
FILE REFERENCE: IPZ02021D2
CURRENT APPLICATION NUMBER: US/09/940,497
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 09/241,376
PRIOR FILING DATE: 1999-02-02
PRIOR APPLICATION NUMBER: US 08/744,138
PRIOR FILING DATE: 1996-11-05
PRIOR APPLICATION NUMBER: US 08/461,030
PRIOR FILING DATE: 1995-06-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 149
TYPE: PRT
ORGANISM: Homo sapiens
US-09-940-497-2

Query Match 20.2%; Score 138.5; DB 9; Length 149;
Best Local Similarity 31.5%; Pred. No. 5.5e-07;
Matches 34; Conservative 22; Mismatches 45; Indels 7; Gaps 3;
Qy 10 PTKICVGCPRDIPNSPELEETLTHITKLNAAENNATYFKIDNVKKARVQQVAGKRYFID 69
Db 30 PQERMVGEGLRDLSPDDPQVKAAQAVASYNMGNSNIIYFPDTHIKAQSOLVAGKRYFID 61
Qy 70 DVARRETTCSKE--SNEELTESCETKLQQ--SLDCNAEYVVVPW 111
Db 90 TMENGSTDRCRTRVTDGHVDLT-TCPLAGAQOEKRCDFEVLVVPWQ 115

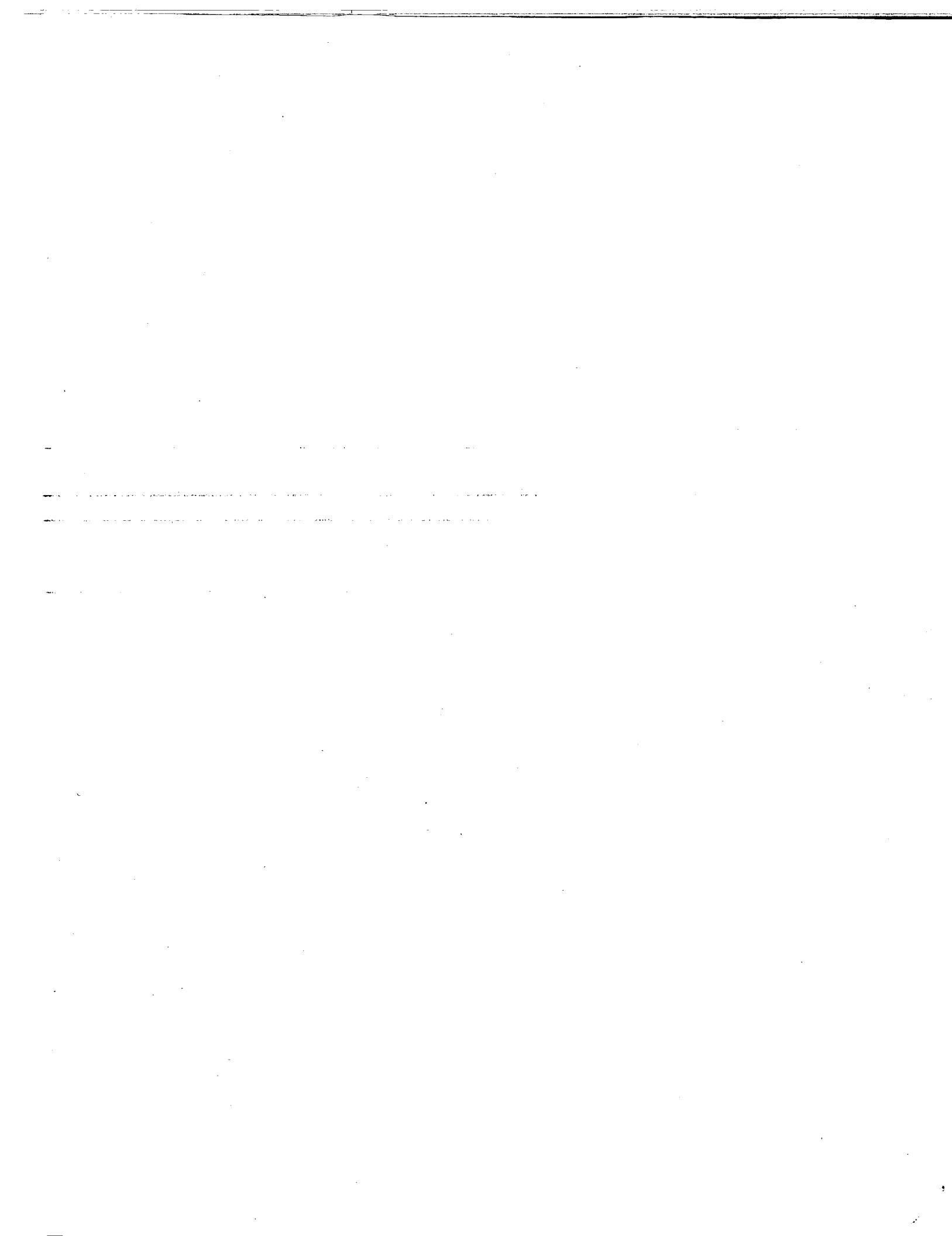
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ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,303
FILING DATE: 21-MAY-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 11321-1-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELELEX: 133521
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO

Query	Match	20.0%	Score 137.5;	DB 8;	Length 112;
Best Local	Similarity	28.8%	Pred. No. 4	9e-07;	
Matches	32;	Conservative	Mismatches	35;	Indels 19;
					Gaps 4;
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12	NEGGQDALSFAVESTFKRSNDAYQSRRVVRARKQWISGMNYFLDVELGRTCTK--S	69			
84	EELTESC-----ETTKLGQSLSIDCNAEYVVPMWEKKIPTVTWNHCE	126			
70	-----OSEOMVYAPNON-----TTNTVKPESO-----TTNTVKPESO	111			

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Job time : 45.704 secs



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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 24, 2004, 14:07:01 ; Search time 14.268 Seconds

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Title: US-10-661-784-1

Perfect score: 660

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 2: /cgm2_6/pctodata/2/iaa/5B.COMB.pep:
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Prev. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6.00	90.9	117	1 US-08-193-114B-1	Sequence 1, Appli
2	5.94	90.0	117	5 PCT-US2-0609-1	Sequence 1, Appli
3	16.9	25.6	178	2 US-08-191-522-1	Sequence 1, Appli
4	16.9	25.6	178	3 US-09-314-777-1	Sequence 2, Appli
5	16.5	25.1	145	2 US-08-332-535-2	Sequence 2, Appli
6	16.5	25.1	145	3 US-09-019-435-2	Sequence 2, Appli
7	16.5	25.1	145	3 US-09-019-435-3	Sequence 3, Appli
8	16.5	25.1	145	3 US-09-431-480-9	Sequence 9, Appli
9	16.5	25.1	145	3 US-09-617-307-9	Sequence 9, Appli
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11	15.5	23.5	27	3 US-08-676-242-11	Sequence 11, Appli
12	14.5	22.0	64	3 US-08-676-242-22	Sequence 22, Appli
13	14.5	22.0	64	3 US-09-002-731-0	Sequence 1, Appli
14	13.8	21.0	121	4 US-09-617-302-8	Sequence 14, Appli
15	13.8	21.0	128	4 US-09-775-932-14	Sequence 12, Appli
16	13.8	21.0	149	2 US-08-461-030C-2	Sequence 2, Appli
17	13.8	21.0	149	3 US-08-744-138-2	Sequence 2, Appli
18	13.8	21.0	149	3 US-09-431-480-8	Sequence 8, Appli
19	13.8	21.0	149	3 US-09-431-480-10	Sequence 10, Appli
20	13.8	21.0	149	3 US-09-617-302-8	Sequence 8, Appli
21	13.8	21.0	149	3 US-09-617-302-10	Sequence 10, Appli
22	13.8	21.0	149	4 US-09-241-376-2	Sequence 2, Appli
23	13.8	21.0	149	4 US-09-940-497-2	Sequence 2, Appli
24	13.6	20.6	112	4 US-08-849-303-16	Sequence 16, Appli
25	13.5	20.5	118	5 PCT-US95-0715-2	Sequence 24, Appli
26	13.4	20.3	148	5 PCT-US95-0715-2	Sequence 2, Appli
27	13.2	20.0	146	3 US-08-676-242-15	Sequence 15, Appli

ALIGNMENTS

RESULT 1
 US-08-193-114B-1
 ; Sequence 1, Application US/08193114B
 ; Patent No. 5472945
 ; GENERAL INFORMATION:
 ; APPLICANT: Schmaier, Alvin H.
 ; ATTORNEY/AGENT: Jiaiang, Yongping
 ; TITLE OF INVENTION: Preparation of Blood
 ; PREPARATION AND INHIBITION OF PLATELET ACTIVATION
 ; TITLE OF INVENTION: Pressure and Inhibition of Platelet Activation
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Seidel, Gonda, Lavorgna &
 ; ADDRESS: Monaco, P.C.
 ; STREET: 1800 Two Penn Center Plaza
 ; CITY: Philadelphia
 ; STATE: Pennsylvania
 ; COUNTRY: U.S.A.
 ; ZIP: 19102
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 720 kb
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: Wordperfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/193,114B
 ; FILING DATE: 9 February 1994
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: U.S. Application
 ; FILING DATE: 13 August 1991
 ; ATTORNEY/AGENT: INFORMATION:
 ; NAME: Monaco, Daniel A.
 ; REGISTRATION NUMBER: 30,480
 ; REFERENCE/OCKET NUMBER: 6056-137 CI1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (215) 568-8383
 ; TELEFAX: (215) 568-3549
 ; TELEX: NO. 5472945E
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 117 amino acids
 ; TYPE: peptide
 ; TOPOLOGY: linear
 ; US-08-193-114B-1
 ; Query Match 90.9%; Score 600; DB 1; Length 117;
 ; Best Local Similarity 100.0%; Prod. No. 5,8e-59;
 ; Matches 112; Conservative 0; Missmatches 0;
 ; Indexes 0; Gaps 0;

RESULT 2
PCT-US92-06809-1

; Sequence 1; Application PC/TUS9206809

; GENERAL INFORMATION:

; APPLICANT: Schmaier, Alvin H.

; APPLICANT: Jiang, Yongping

; TITLE OF INVENTION: Modulation of Blood

; TITLE OF INVENTION: Pressure by Altering Bradykinin Levels

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSSEE: Temple University - Of the

; STREET: 406 University Services

; STREET: Building

; CITY: Philadelphia

; STATE: Pennsylvania

; COUNTRY: U.S.A.

; ZIP: 19122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/066809

; FILING DATE: 19910813

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. Application

; APPLICATION NUMBER: Serial No. 744,545

; FILING DATE: 13 August 1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Monaco, Daniel A.

; REGISTRATION NUMBER: 30,480

; REFERENCE/DOCKET NUMBER: 6056-137

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 568-9383

; TELEX: (215) 568-5549

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 117 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: Linear

US-08-791-322-1

Query Match 90 %; Score 594; DB 5; Length 117;

Best Local Similarity 98.2%; Pred. No. 2.7e-58;

Matches 110; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
US-09-314-777-1

; Sequence 1; Application US/09314777

; Patent No. 6110686

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Goli, Surya K.

; TITLE OF INVENTION: PROTEIN

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

RESULT 3
US-09-791-522-1

; Sequence 1; Application US/08791522

; Patent No. 5935817

```

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ For Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/314,777
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/791,522
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0193 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: 30443
US-09-314-777-1

Query Match          25.6% Score 169; DB 3
Best Local Similarity 32.5%; Pred. No. 5.4e-1
Matches   39; Conservative 22; Mismatches
Qy      9 TKIVCGCPRDPTNTNSPELEETLTHTLTKNAENNAT
Db      54 SRVTKPGPFKTTKTNDCGCVLQAARYSERVEKFKNCTNDM
Qy      69 FVARETGSCKSNEELDEESCE---TKYKLGSIDNA
Db      114 VEIGRTICKKNGHRLR-DDCDDFQTNTLKTQTLSCYS

RESULT 5
US-08-832,535-2
Sequence 2, Application US/08832535
Patent No. 591365B
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: LI, HAODONG
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER L
TITLE OF INVENTION: HUMAN CYSTATHIENYLIC ACID
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850
COMPILER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,535
FILING DATE: 03-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KIMBALL, PAUL C.
REGISTRATION NUMBER: 34,610
REFERENCE/DOCKET NUMBER: PF265
TELECOMMUNICATION INFORMATION:

```

Qy 69 FVARETCSKESNEELTESCB---TKRLGQSLDNCNAEVVVVFWERKI-YPTVNC 118
 Db. 92 VEIGRTICKNQHLRL-DDCDFQTNTLKTQLSCYSEWVWVWLQHFEVVPVLR 144

RESULT 7

Sequence 3, Application US/0919485
 Patent No. 6066617

GENERAL INFORMATION:

APPLICANT: Li, Haodong
 APPLICANT: Yu, Guo-Jiang
 APPLICANT: Gentz, Reiner

TITLE OF INVENTION: Cystatin F

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: MD

COUNTRY: US

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ParentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/019,485

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Robert H.

REGISTRATION NUMBER: 30,446

REFERENCE/DOCKET NUMBER: PP265P1

INFORMATION:

TELEPHONE: 3013098504

TELEFAX: 3013098439

SEQUENCE INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 145 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-019-485-3

Qy 69 FVARETCSKESNEELTESCB---TKRLGQSLDNCNAEVVVVFWERKI-YPTVNC 118
 Db. 92 VEIGRTICKNQHLRL-DDCDFQTNTLKTQLSCYSEWVWVWLQHFEVVPVLR 144

RESULT 8

Sequence 9, Application US/09431480
 Patent No. 6235708

GENERAL INFORMATION:

APPLICANT: Holloway, James L.

TITLE OF INVENTION: TESTIS SPECIFIC CYSTATIN-LIKE PROTEIN CYSTATIN T

FILE REFERENCE: 98-72

CURRENT APPLICATION NUMBER: US/09/431,480

CURRENT FILING DATE: 1999-11-01

EARLIER APPLICATION NUMBER: 60/109,217

Qy 69 FVARETCSKESNEELTESCB---TKRLGQSLDNCNAEVVVVFWERKI-YPTVNC 118
 Db. 92 VEIGRTICKNQHLRL-DDCDFQTNTLKTQLSCYSEWVWVWLQHFEVVPVLR 144

RESULT 9

Sequence 9, Application US/09617302

Patent No. 624529

GENERAL INFORMATION:

APPLICANT: Holloway, James L.

TITLE OF INVENTION: TESTIS SPECIFIC CYSTATIN-LIKE PROTEIN CYSTATIN T

FILE REFERENCE: 98-72 CI

CURRENT APPLICATION NUMBER: US/09/617,302

PRIOR APPLICATION NUMBER: 09/431,480

PRIOR FILING DATE: 1999-11-01

PRIOR APPLICATION NUMBER: 60/109,217

PRIOR FILING DATE: 1998-11-20

PRIOR APPLICATION NUMBER: 60/156,382

PRIOR FILING DATE: 1999-09-28

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 9

LENGTH: 145

TYPE: PRT

ORGANISM: Homo sapiens

US-09-617-302-9

Qy 69 FVARETCSKESNEELTESCB---TKRLGQSLDNCNAEVVVVFWERKI-YPTVNC 118
 Db. 92 VEIGRTICKNQHLRL-DDCDFQTNTLKTQLSCYSEWVWVWLQHFEVVPVLR 144

RESULT 10

Sequence 2, Application US/09528436B

Patent No. 657645

GENERAL INFORMATION:

APPLICANT: Li, et al.

TITLE OF INVENTION: Human Cystatin F

FILE REFERENCE: PF265P1D1

CURRENT APPLICATION NUMBER: US/09/528,436B

CURRENT FILING DATE: 2000-03-17

PRIOR APPLICATION NUMBER: 09/019,485

Qy 69 FVARETCSKESNEELTESCB---TKRLGQSLDNCNAEVVVVFWERKI-YPTVNC 118
 Db. 92 VEIGRTICKNQHLRL-DDCDFQTNTLKTQLSCYSEWVWVWLQHFEVVPVLR 144

RESULT 11
 PRIORITY FILING DATE: 1998-01-29
 PRIORITY APPLICATION NUMBER: 08/332,535
 PRIORITY FILING DATE: 1999-04-03
 PRIORITY APPLICATION NUMBER: 50/014,795
 PRIORITY FILING DATE: 1996-04-03
 PRIORITY APPLICATION NUMBER: US 16
 NUMBER OF SEQ ID NOS: 16
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 2
 LENGTH: 145
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-528-436B-2
 Query Match 25.1%; Score 165.5; DB 4; Length 145;
 Best Local Similarity 32.5%; Pred. No. 1e-10; Indels 5; Gaps 3;
 Matches 37; Conservative 22; Mismatches 0;
 OTHER INFORMATION: Description of Artificial Sequence: From human
 OTHER INFORMATION: Kininogen heavy chain
 US-08-676-242-22
 Query Match 22.0%; Score 145; DB 3; Length 64;
 Best Local Similarity 100.0%; Pred. No. 6.3e-09;
 Matches 25; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;
 OTHER INFORMATION: Bradykinin Analogs As Selective Inhibitors of Cell
 QY 99 CNAEVVVPWEEKIYPTVNQPLGM 123
 Db 1 CNAEVVVPWEEKIYPTVNQPLGM 25

RESULT 12
 US-08-676-242-11
 Sequence 11, Application US/08676242C
 Patent No. 6143719
 GENERAL INFORMATION:
 APPLICANT: The Regents of the University of Michigan
 ATTORNEY: Schmaier, Alvin H.
 TITLE OF INVENTION: Bradykinin Analogs As Selective Thrombin Inhibitors
 FILE REFERENCE: 8820-2 US
 CURRENT APPLICATION NUMBER: US/08/676,242C
 CURRENT FILING DATE: 2000-07-16
 EARLIER APPLICATION NUMBER: 60/000,095
 EARLIER FILING DATE: 1995-06-09
 EARLIER APPLICATION NUMBER: PCT/US96/09940
 EARLIER FILING DATE: 1996-06-07
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 11
 LENGTH: 27
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: Description of Artificial Sequence: Bradykinin
 OTHER INFORMATION: Description of Artificial Sequence: Bradykinin
 analog
 US-08-676-242-11
 Query Match 23.5%; Score 155; DB 3; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.6e-10;
 Matches 27; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;
 OTHER INFORMATION: Description of Artificial Sequence: Bradykinin
 analog

RESULT 13
 US-09-402-732-1
 Sequence 1, Application US/09402732
 Patent No. 6251855
 GENERAL INFORMATION:
 APPLICANT: Schmaier, Alvin H.
 ATTORNEY: Hasan, A.K. Ahmed
 TITLE OF INVENTION: Bradykinin Analogs As Selective Inhibitors of Cell
 FILE REFERENCE: 8820-3
 CURRENT APPLICATION NUMBER: US/09/402,732
 CURRENT FILING DATE: 1999-12-01
 PRIOR APPLICATION NUMBER: 60/046,085
 PRIOR FILING DATE: 1997-04-23
 PRIOR APPLICATION NUMBER: PCT/US98/08015
 PRIOR FILING DATE: 1998-04-21
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 1
 LENGTH: 64
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Segment of
 Cystatins
 OTHER INFORMATION: Human kininogen (residues 333-396 thereof)
 US-09-402-732-1
 Query Match 22.0%; Score 145; DB 3; Length 64;
 Best Local Similarity 100.0%; Pred. No. 6.3e-09;
 Matches 25; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;
 OTHER INFORMATION: Description of Artificial Sequence: Segment of
 Cystatins
 QY 99 CNAEVVVPWEEKIYPTVNQPLGM 123
 Db 1 CNAEVVVPWEEKIYPTVNQPLGM 25

RESULT 14
 US-09-775-932-14
 Sequence 14, Application US/09775932
 Patent No. 6534477
 GENERAL INFORMATION:
 APPLICANT: University of British Columbia
 TITLE OF INVENTION: Production and use of Modified Cystatins
 FILE REFERENCE: 58069
 CURRENT APPLICATION NUMBER: US/09/775,932
 CURRENT FILING DATE: 2001-02-02
 PRIOR APPLICATION NUMBER: CA99/00717
 PRIOR FILING DATE: 1999-08-05

RESULT 15
 US-08-676-242-22
 Sequence 22, Application US/08676242C
 Patent No. 6143719
 GENERAL INFORMATION:
 APPLICANT: The Regents of the University of Michigan
 ATTORNEY: Schmaier, Alvin H.
 TITLE OF INVENTION: Bradykinin Analogs As Selective Thrombin Inhibitors
 FILE REFERENCE: 8820-2 US
 CURRENT APPLICATION NUMBER: US/08/676,242C
 CURRENT FILING DATE: 2000-07-16
 EARLIER APPLICATION NUMBER: 60/000,095
 EARLIER FILING DATE: 1995-06-09
 EARLIER APPLICATION NUMBER: PCT/US96/09940
 EARLIER FILING DATE: 1996-06-07
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 11
 LENGTH: 27
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Bradykinin
 analog

PRIOR APPLICATION NUMBER: 60/095,503
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 121
TYPE: PRT
ORGANISM: Homo sapiens

Query Match	21	0%	Score 138 5;	DB 4;	Length 121;
Best Local Similarity	31.5%	Pred. No.	7.7e-08;		
Matches	34;	Mismatches	22;	Indels	7;
Matches	34;	Conservative	22;	Gaps	3;
8	PTKIKVGCPRDIPTNSPEELTLTITKINAENNATPYFKIDNPKKARVQVAGKKYPI	67			
Y	: :				
2	FQERVGEUDLSPPDQVORAAQAVASTYNGSISIYFERTDIIKIKAQSOLVAKIYFL	61			
b	: :				
68	DVFARETTCSKE---SNEELTESSCETKLGG--SLDCNAEVTWVPMW	109			
Y	: :				
b	: :				

SEQUENCE 15
S-19-775-932-12
Sequence 12, Application US/09775932
Patent No. 6534477
GENERAL INFORMATION:
APPLICANT: University of British Columbia
TITLE OF INVENTION: Production and use of Modified Cystatins
FILE REFERENCE: 58069
CURRENT APPLICATION NUMBER: US/09/775,932
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: CA99/00717
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 60/095,503
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ_ID NO 12
LENGTH: 128
TYPE: PRT
ORGANISM: Homo sapiens

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Query Match      21.0%; Score 138.5; DB 4; Length 128;
Best Local Similarity 31.5%; Pred. No. 8.3e-08;
Matches 34; Conservative 22; Missmatches 45; Indels 7; Gaps 3;

8 PTKIVGGCPBDIPNNPSLEETLTITKINAENNATYEFIDNKKARVQVAGKXIFI 67
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
9 PQBERMVGELRDLSDPDPOQKAQAAVASYNNGCSNSITYFRDTHIIAQSQLVAGGKXFL 68

68 DVARETTCSKE ---SNEELTSCTERKLQG -SLDGNAEVYYVVPWE 109
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
69 TMDNCSTMCRKPTWMDPDTI MDRY AGCAGKDKI DPKDTI WDTI 115

```

Search completed: September 24, 2004, 14:11:36
Job time : 27,268 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 24, 2004, 14:02:27 ; Search time 49.692 Seconds
 (without alignments)

699.375 Million cell updates/sec

Title: US-10-661-784-1

Perfect score: 660

Sequence: 1 GKDVFQPPTKICVCPRDIP.....YVVPWERKITYPTVNQCPFLGM 123

Scoring table: BLOSUM62

GapOp 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters:

1586107

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database :

- 1: _Geneseq_29Jat04:*
- 2: _GeneseqP198S:*
- 3: _GeneseqP200S:*
- 4: _GeneseqP200S:*
- 5: _GeneseqP200S:*
- 6: _GeneseqP200S:*
- 7: _GeneseqP200S:*
- 8: _GeneseqP200S:*

ALIGNMENTS

RESULT 1

ID AAY95426

standard; Peptide; 123 AA.

XX

AC AAY95426;

XX

DT 25-SEP-2000 (first entry)

XX

DE Human high mol.wt. Kininogen domain 3.

XX

KW Anti-angiogenic angiogenesis; inhibitor: kininogen; homologue:
 endothelial cell proliferation; apoptosis; cancer; ocular disorder;
 rheumatoid arthritis; cytosatic; antiarthritic; antirheumatic; therapy;

human; D3 Peptide.

XX

OS Homo sapiens.

XX

PN WO20035407-A2.

XX

PD 22-JUN-2000.

XX

PF 02-DEC-1999;

XX

99WO-US028465.

XX

PR 16-DEC-1998;

XX

PA (UTEM) UNIV TEMPLE.

XX

PA (MCCR/) MCCRAE R K.

XX

PI McCrae RK;

XX

DR WPI; 2000-442247/38.

XX

PT Composition for inhibiting angiogenesis and endothelial cell

proliferation, inducing endothelial cell apoptosis and treating cancer,

rheumatoid arthritis, and ocular disorders comprises a kininogen domain 3

analog.

XX

Disclosure; Page 4; 44pp; English.

XX

PS

CC

Aaw69734 Human cys
 Aay5418 Anti-angi
 Ab3345 Human cys
 Aw32323 Mature hu
 Aw31902 Human cys
 Ay5708 Human cys
 Aae02410 Human cys
 Aae04439 Human cys
 Add14098 Human src
 Aay0287 Secreted
 Ada5154 Human pol
 Aay95408 Anti-angi
 Ab37446 Human kin
 Aw8910 Mouse IMC
 Aw54335 Bradykini
 Aay95425 Anti-angi
 Aw5341 Bradykini
 Aay77418 Kininogen
 Aay81200 Human mut
 Aay81189 Human mut

SUMMARIES

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB	ID	Description
1	660	100.0	123	3	AY95426		Aay95426 Human hig
2	660	100.0	304	6	ABP70801		Abp70801 Human ext
3	660	100.0	322	6	ABP70799		Abp70799 Human ext
4	660	100.0	329	6	ABP72044		Abp72044 Human pro
5	660	100.0	358	6	ABP70800		Abp70800 Human ext
6	660	100.0	390	6	ABU99149		Abu99149 Novel hum
7	660	100.0	398	6	ABU9143		Abu9143 Novel hum
8	660	100.0	427	8	ADE16864		Adet6864 Human pro
9	660	100.0	615	6	ABU99144		Abu99144 Novel hum
10	660	100.0	626	5	ABP78707		Abp78707 Human hig
11	660	100.0	644	4	ABG21101		Abg21101 Novel hum
12	660	100.0	644	4	ABT78710		Abt78710 Human hig
13	660	100.0	644	6	ABU99150		Abu99150 Novel hum
14	660	100.0	644	6	ABU99145		Abu99145 Novel hum
15	628	95.2	122	3	AAB7447		Human kin
16	594	90.0	117	2	AAR33350		Domain 3
17	589.5	89.3	435	4	ABG21105		Abg21105 Novel hum
18	477	72.3	436	1	AAP20257		Aap20257 Human DIT
19	453	68.6	437	6	ABR41202		Abr41202 Human DIT
20	450	68.2	434	1	AAP0633		Aap0633 Bradykini
21	409	62.0	235	4	ABG6077		Abg6077 Human DIT
22	320.5	48.6	248	4	ABG21102		Abg21102 Novel hum
23	316	47.9	369	4	ABG21099		Abg21099 Novel hum
24	190	28.8	305	4	ABG21100		Abg21100 Novel hum
25	175	26.5	167	2	AAN98907		Aan98907 Mouse IMC

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Query

Match

Length

DB

ID

Aaw69734 Human cys
 Aay5418 Anti-angi
 Ab3345 Human cys
 Aw32323 Mature hu
 Aw31902 Human cys
 Ay5708 Human cys
 Aae02410 Human cys
 Aae04439 Human cys
 Add14098 Human src
 Aay0287 Secreted
 Ada5154 Human pol
 Aay95408 Anti-angi
 Ab37446 Human kin
 Aw8910 Mouse IMC
 Aw54335 Bradykini
 Aay95425 Anti-angi
 Aw5341 Bradykini
 Aay77418 Kininogen
 Aay81200 Human mut
 Aay81189 Human mut

The present sequence is that of domain 3 of human high mol.wt. kininogen

(HR). The invention provides peptides (see AAY95405-4) that are

analogaues of certain sites in the HK domain 3, specifically An275-

Lys82, Cys246-Cys249, Leu331-Tyr38 and Tyr299-Ser34. The peptides, in

which native Cys residues may be replaced by Ala residues, inhibit

endothelial cell proliferation and may also induce endothelial cell

apoptosis. Compositions including the peptides are used in claimed

methods for inhibiting angiogenesis, inhibiting endothelial cell

proliferation, and inducing endothelial cell apoptosis. Cancer,

proteins (EXMES-1 to -28; ABP7074-ABP70801) and their coding sequences (AC42361-AC42388). The proteins are useful for preparing a composition for diagnosing or treating a disease or condition associated with decreased expression or overexpression of functional EXMES e.g. autoimmune/inflammatory disorders, diabetes, endocrine disorders or

XX	SQ	Sequence 322 AA;	Query Match	Score 660; DB 6;	Length 322;
			Best Local Similarity	100.0%;	Pred. No. 8.7e-66;
			Matches 123; Conservative	0; Mismatches 0;	Indels 0; caps 0;
Qy	1	GKDFYQPPTKICVGCRDIPNTNSPELEETLTHITCLNAENNATYFKIDNVKKARYQQV	60		
Db	148	GKDFYQPPTKICVGCRDIPNTNSPELEETLTHITCLNAENNATYFKIDNVKKARYQQV	207		
Qy	61	AGKXYFIDFVARETTSKESNEELTSCETRKLQGSDUDCNAEAEVYYFWERKLYPTVNQCP	120		
Db	208	AGKXYFIDFVARETTSKESNEELTSCETRKLQGSLDCNAEAEVYYFWERKLYPTVNQCP	267		
Qy	121	LGM 123			
Db	268	LGM 270			

PI Marquis JP, Yao MG, Richardson TW, Tang TY, Jin P, Chien D;
PI Bhattia U, Burill JD, Lee S, Blake JJ, Ho A, Zheng W;
XX

New human protein modification and maintenance molecules (PMM), useful for diagnosis, prevention and treatment of diseases.

The present invention relates to the isolation of human serum with the aberrant PNM expression e.g. cancer, atherosclerosis, or infections.

modification and maintenance molecules (PMM), and the polynucleotide sequences encoding them. A total of 40 PMM polypeptides (designated PMM-1 to PMM-40) are disclosed. The sequences of the invention are useful for diagnosing a condition or disease associated with the expression of PMM in a subject, preparing a polyclonal or monoclonal antibody, and generating an expression profile of a sample containing the polynucleotides. The diseases or conditions associated with decreased expression or overexpression of PMM are cell proliferation disorders (e.g. cancer, atherosclerosis), neurological disorders (e.g. epilepsy, Huntington's disease, stroke), immune/inflammatory disorders, (e.g. AIDS, allergies), developmental disorders (e.g. hypothyroidism, Cushing's syndrome), gastrointestinal or epithelial disorders, and infections. The PMM polypeptides or their fragments are useful in screening compounds for effectiveness as agonists or antagonists of the polypeptides, or in altering the expression of the target polynucleotide and compounds that specifically bind to, or modulate the activity of the polypeptide. ABU92021-ABU92060 represent the human PMM polypeptides of the invention.

query Match 100.0%; Score 660; DB 6; Length 329;
 best Local Similarity 100.0%; Pred. No. 9e-66;
 matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1	GKDFYQOPTKICVGCCRDIPTNSPLEETLTITKLNAENNATYFKIDNVKCARVQVV	60
155	GKDfYQOPTKICVGCCRDIPTNSPLEETLTITKLNAENNATYFKIDNVKCARVQVV	214
61	AGKKYFIDFVARETTCSKESNEELTESCETKLGQLSDCNAAEVVVPMEKKIYPTVNCP	120
215	AGKKYFIDFVARETTCSKESNEELTESCETKLGQLSDCNAAEVVVPMEKKIYPTVNCP	274
121	LGM 123	
275	LGM 277	

WILT 5
 70800 ABP70800 standard; protein; 358 AA.
 ABP70800;

^

26-AUG-2003 (first entry)

Human extracellular messenger, EXMES-27.
 Human; extracellular messenger; EXMES; cytosstatic; antidiabetic; immunosuppressive; autoimmune disorder; inflammatory disorder; diabetes; endocrine disorder; cancer.
 Homo sapiens.
 WO2003018612-A2.
 06-MAR-2003.
 22-AUG-2002; 2002WO-US027213.
 24-AUG-2001; 2001US-0314811P.
 14-DEC-2001; 2001US-034584P.
 18-JAN-2002; 2002US-035095P.
 11-MAR-2002; 2002US-0363432P.
 15-MAR-2002; 2002US-036407P.
 05-APR-2002; 2002US-0370761P.
 24-JUN-2002; 2002US-0391378P.

PA	(INCY-) INCYTE GENOMICS INC.	04-JUN-2002; 2002WO-US017428.
XX	Duggan BM, Lee S, Baughn MR, Hafalia AJA, Wallia NK, Elliott VS;	XX
PI	Lee SY, Khare R, Wilson AD, Jin P, Hawkins PR, Tang YT, Burford N;	PR 04-JUN-2001; 2001US-0295607P.
PI	Ding L, Yao MG, Becha SD, Tran UK, Chien D, Zebardadian Y;	PR 04-JUN-2001; 2001US-0295611P.
PI	Ramkumar TW, Kable AE, Chang H, Swarnakar A, Lehr-Masison PM;	PR 06-JUN-2001; 2001US-0296404P.
PI	Ramkumar J;	PR 07-JUN-2001; 2001US-0296418P.
XX	DR; 2003-278643/47.	PR 14-JUN-2001; 2001US-0298285P.
DR	N-PSDB; ACC12387.	PR 15-JUN-2001; 2001US-0298556P.
XX	New human extracellular messenger (EXMES) polypeptide, useful for preparing a composition for treating a disease associated with decreased expression or overexpression of functional EXMES e.g. autoimmune disorders or cancer.	PR 21-JUN-2001; 2001US-0299949P.
PT	The present invention relates to novel human extracellular messenger proteins (EXMES-1 to -28; ABP7014 -ABP7081) and their coding sequences (ACC4261-ACC42368). The proteins are useful for preparing a composition for diagnosing or treating a disease or condition associated with decreased expression or overexpression of functional EXMES e.g. autoimmune/inflammatory disorders, diabetes, endocrine disorders or cancer.	PR 26-JUN-2001; 2001US-0300833P.
PS	Claim 1; Page 206; 224pp; English.	PR 28-JUN-2001; 2001US-0301550P.
CC	The present invention relates to novel human extracellular messenger proteins (EXMES-1 to -28; ABP7014 -ABP7081) and their coding sequences (ACC4261-ACC42368). The proteins are useful for preparing a composition for diagnosing or treating a disease or condition associated with decreased expression or overexpression of functional EXMES e.g. autoimmune/inflammatory disorders, diabetes, endocrine disorders or cancer	PR 13-AUG-2001; 2001US-0311972P.
CC	Sequence 358 AA;	PR 27-AUG-2001; 2001US-0315071P.
CC	Best Local Similarity 100.0%; Score 660; DB 6; Length 358;	PR 29-AUG-2001; 2001US-0315650P.
CC	Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	PR 14-SEP-2001; 2001US-0322293P.
CC	Query Match 100.0%; Pred. No. 1e-65;	PR 17-SEP-2001; 2001US-0322706P.
CC	Score 660; DB 6; Length 358;	PR 14-DEC-2001; 2001US-0341186P.
CC	XX	PR 28-FEB-2002; 2002US-0361189P.
CC	XX	PR 12-MAR-2002; 2002US-0316367P.
CC	XX	PR 12-MAR-2002; 2002US-0316367P.
CC	XX	PR 03-JUN-2002; 2002US-00363676.
CC	XX	PR 03-JUN-2002; 2002US-00363676.
CC	PA (CUBA-) CURAGEN CORP.	XX
CC	XX	PR WPI-2003-140627/13.
CC	XX	DR N-PSDB; AC03653.
CC	XX	PT New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or pharmacogenomics.
CC	XX	CC Claim 1; Page 147; 332pp; English.
CC	XX	CC The invention describes an isolated polypeptide (I) comprising any of 27 mature form of them, a sequence that is at least 95 % identical to them, or a sequence having one or more conservative substitutions in them. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with human disease selected from a pathology associated with the polypeptide. The NOVX polypeptides, polynucleotides and antibodies are useful in treating or preventing NOVX-associated disorders, e.g. cardiomopathy, atherosclerosis, cancer, immune disease, AIDS, obesity, asthma, hematopoietic disorders, Parkinson's disease, Alzheimer's disease, infections, multiple sclerosis, cancer-associated cachexia, and other wasting disorders associated with chronic diseases. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haemopoiesis, wound healing and angiogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or diagnostic methods. The nucleic acids are further used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The polypeptides are also useful as vaccines, and this is the amino acid sequence of a novel human G-protein coupled receptor related protein NOV12g.
CC	XX	CC Query Match 100.0%; Score 660; DB 6; Length 390;
CC	XX	CC Best Local Similarity 100.0%; Pred. No. 1.e-65;
CC	XX	CC Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC	XX	CC OS Homo sapiens.
CC	XX	CC PN WO20029116-A2.
CC	XX	CC PD 12-DEC-2002.
CC	XX	CC

XX WPI: 2004-031227/03.
 DR N-PSDB; ADE7663.
 XX Composition comprising several cDNAs that are differentially expressed in PT treated human C3A liver cell cultures, useful for treating liver disorders.
 XX Claim 1; SEQ ID NO 29; 41pp; English.
 The invention relates to a composition comprising several cDNAs that are differentially expressed in a liver disorder. The composition is useful for treating liver disorder such as hyperlipidaemia, hypertension, type II diabetes, tumours of the liver and disorders of the inflammatory and immune response. The composition is useful for a high-throughput method of screening several molecules or compounds to identify a ligand which specifically binds a cDNA. A protein encoded by the cDNA is useful for a high-throughput method for using a protein to screen several molecules or compounds to identify at least one ligand which specifically binds the protein which involves combining the protein encoded by the cDNA with several of molecules or compounds under conditions to allow specific binding, and detecting specific binding between the protein and a molecule or compound, therefore identifying a ligand which specifically binds the protein. The composition is useful for detecting and quantifying differential gene expression, can be used in gene therapy, to formulate prognosis and to design a treatment regimen and to monitor the efficacy of treatment. The present sequence represents the amino acid sequence of a protein encoded by a cDNA differentially expressed in a liver disorder.

XX Sequence 427 AA;
 Query Match 100.0%; Score 660; DB 8; Length 427;
 Best Local Similarity 100.0%; Pred. No. 1.3e-65;
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SQ 1 GRDFVQPTTKICVGCPDPIDPTNSPELDTLTITKLNAAATTYFKIINVKKARVQVY 60
 DB 253 GRDFVQPTTKICVGCPDPIDPTNSPELDTLTITKLNAAATTYFKIINVKKARVQVY 312
 Qy 61 AGKRYFIDFVARETTCSKSNEBELTESCTKLQGQLDCNAEVTVTPWEEKKIYPTVNCOF 120
 DB 313 AGKRYFIDFVARETTCSKSNEBELTESCTKLQGQLDCNAEVTVTPWEEKKIYPTVNCOF 372

Qy 121 LGM 123
 Db 373 LGM 375

RESULT 9
 ABU99144 ID ABU99144 standard; protein: 615 AA.
 AC ABU99144;
 XX 01-AUG-2003 (first entry)

XX Novel human GPCR related protein NOV12b.

XX Human; G-protein coupled receptor related protein; GPCR related protein; DE immunomodulator; anti-HIV; anorectic; antiasthmatic; haemostatic; XX cytostatic; cariant; antiarteriosclerotic; antidiabetic; XX NOVX-associated disorder; cardiomopathy; nootropic; gene therapy; vaccine; XX diabetes; immune disorder; AIDS; obesity; asthma; XX haemopoietic disorder; Parkinson's disease; Alzheimer's disease; infection; multiple sclerosis; cancer-associated cachexia; XX wasting disorder; chronic disease; neurogenesis; cell differentiation; XX cell proliferation; haematopoiesis; wound healing; angiogenesis; XX chromosome mapping; tissue typing; preventive medicine; pharmacogenomic. OS Homo sapiens.

XX PN WO200299116-A2.
 XX PR 04-JUN-2001; 2001US-0295607P.
 XX PR 04-JUN-2001; 2001US-029561P.
 XX PR 06-JUN-2001; 2001US-0296404P.
 XX PR 06-JUN-2001; 2001US-0296418P.
 XX PR 14-JUN-2001; 2001US-0298285P.
 XX PR 15-JUN-2001; 2001US-0298556P.
 XX PR 21-JUN-2001; 2001US-0291949P.
 XX PR 26-JUN-2001; 2001US-0300883P.
 XX PR 28-JUN-2001; 2001US-0301550P.
 XX PR 13-AUG-2001; 2001US-0311722P.
 XX PR 27-AUG-2001; 2001US-0315071P.
 XX PR 29-AUG-2001; 2001US-0315660P.
 XX PR 14-SEP-2001; 2001US-0322293P.
 XX PR 17-SEP-2001; 2001US-0322706P.
 XX PR 14-DEC-2001; 2001US-0341186P.
 XX PR 28-FEB-2002; 2002US-0361189P.
 XX PR 12-MAR-2002; 2002US-0363673P.
 XX PR 12-MAR-2002; 2002US-0363676P.
 XX PR 03-JUN-2002; 2002US-00363676.
 XX PA (CURA-) CURAGEN CORP.
 XX PI Anderson DW, Baumgartner JC, Boldog EL, Caaman SJ, Edinger SR, Li L, Gangolli EA, Gerlach VL, Gorman L, Guo X, Hjalt T, Kekuda R, Li L, Macdougall JR, Malyanikar UM, Millat I, Padigaru M, Paturajan M, Pena CEA, Rasteili L, Shimkets RA, Stone DJ, Spytek KA, Vernet CAM, Voss EZ, Zethusen BD.
 XX WPI: 2003-140627/13.
 XX DR N-PSDB; ACD03648.

XX New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or pharmacogenomics.
 XX PS Claim 1; Page 144; 332pp; English.
 XX The invention describes an isolated polypeptide (I) comprising any of 27 CC mature form of them, a sequence that is at least 95 % identical to them, or a sequence having one or more conservative substitutions in them. The CC polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease selected from a pathology CC associated with the polypeptide. The NOVX polypeptides, polynucleotides CC and antibodies are useful in treating or preventing NOVX-associated CC disorders, e.g. cardiomyopathy, atherosclerosis, cancer, diabetes, immune CC disorders, AIDS, obesity, asthma, haemopoietic disorders, Parkinson's CC disease, Alzheimer's disease, infections, multiple sclerosis, cancer- CC associated cachexia, and other wasting disorders associated with chronic CC diseases. The nucleic acids and polypeptides may also be used as targets CC for the identification of small molecules that modulate or inhibit e.g. CC neurogenesis, cell differentiation, proliferation, haemopoiesis, CC wound healing and angiogenesis, in gene therapy, in generation of CC therapeutic or diagnostic methods. The nucleic acids are further used as CC hybridisation probes, in chromosome mapping, tissue typing, preventive CC medicine, and pharmacogenomics. The polypeptides are also useful as CC vaccines. This is the amino acid sequence of a novel human G-protein CC coupled receptor related protein NOVX
 XX Sequence 615 AA;

XX SQ Query Match 100.0%; Score 660; DB 6; Length 615;
 XX Best Local Similarity 100.0%; Pred. No. 2.1e-65;
 XX Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification. Note: The sequence data for this electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

XX

Sequence 644 AA;

Query Match 100.0%; Score 660; DB 4; Length 644;
Best Local Similarity 100.0%; Pred. No. 2.3e-65;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GKDFOQPETKICVGCPRDPTNSPELEBTLTTIKLNAAENNATFYFKIDNVKARQVV 60
Db 253 GKDFOQPETKICVGCPRDPTNSPELEBTLTTIKLNAAENNATFYFKIDNVKARQVV 312
QY 61 AGKKYFIDFVARETTCSKESNBDTSETKRLGQSLDCNAEVYYVPPWEEKIYPTVNQCP 120
Db 313 AGKKYFIDFVARETTCSKESNBDTSETKRLGQSLDCNAEVYYVPPWEEKIYPTVNQCP 372
QY 121 LGM 123
Db 373 LGM 375

XX

18-JUL-2002 (first entry)

DE Human high molecular weight kininogen (HK) protein.

XX

Human; kininogen; high molecular weight kininogen; HK; D5 domain; D5 receptor; angiogenesis; endothelial cell; cytostatic; antitumour; antiatherosclerotic; vasotropic; vulnerary; tranquilliser; thrombotic; ophthalmological; gynaecological; antiulcer; antiidiabetic; antiarthritic; antiangiogenic; antiapoptotic; endocrine; apoptosis; gene therapy.

OS Homo sapiens.

XX

Key Location/Qualifiers
FH 1..18
PT /label= signal
PT 19..644

FT Protein

FT Disulfide-bond
FT Disulfide-bond 83.. .614
FT Disulfide-bond 83.. .94
FT Disulfide-bond 107.. .126
FT Disulfide-bond 142.. .145
FT Disulfide-bond 206.. .218
FT Disulfide-bond 229.. .248
FT Disulfide-bond 264.. .267
FT Disulfide-bond 328.. .340
FT Disulfide-bond 351.. .370
FT Domain 402.. .526
FT /label= D5_domain

XX

PN WO200214369-A2.

XX

PD 21-FEB-2002.

XX

24-JUL-2001; 2001WO-US023185.

PR 24-JUL-2000; 2000US-0220194P.
XX PA (ANTE-) ATTENUN LLC.
XX PI Mazar AP, Juarez JC;
XX DR WPI; 2002-3361142.
XX Novel human kininogen D5 domain polypeptides useful for treating conditions associated with endothelial cell migration, proliferation, invasion or angiogenesis, e.g. arthritis, macular degeneration, benign hyperplasia.

XX

PS Disclosure: Fig 1B-E; 84pp; English.

XX The present invention describes an isolated polypeptide (I) that corresponds to the D5 domain of human kininogen, or biologically active peptide fragment, homologue or functional derivative, and which: (a) inhibits angiogenesis; (b) binds to the D5 binding site on endothelial cells (EC); (c) activates signalling pathways leading to the introduction of apoptosis in EC; and/or (d) inhibits the signalling pathway required for maintenance of EC viability. (I) has cytostatic, antitumour, antiatherosclerotic, vasotropic, vulnerary, tranquilliser, thrombotic, ophthalmological, gynaecological, antiulcer, antiidiabetic, antiarthritic, antiangiogenic, antiapoptotic and endocrine, activities. An antibody (IX) specific for an epitope of (I) is useful for inhibiting tumour growth or angiogenesis in a subject. (I), a D5 fusion polypeptide (III) or a dimeric or trimeric fusion polypeptide (III) can be used for inhibiting EC migration, proliferation, invasion, or angiogenesis, or for inducing EC apoptosis. An angiogenic EG-targeting pharmaceutical composition (X) comprising (I), (III), or (III), can be used for treating a subject having a disease or condition associated with undesired EC migration, proliferation, invasion or angiogenesis. (I), (III), or (III) can be used for isolating a D5 domain binding molecule from a complex mixture and for isolating or enriching cells expressing D5 domain binding sites from a cell mixture. The present sequence represents the human high molecular weight kininogen (HK) protein, which is given in the exemplification of the present invention

XX

SQ Sequence 644 AA;

Query Match 100.0%; Score 660; DB 5; Length 644;
Best Local Similarity 100.0%; Pred. No. 2.3e-65; Mismatches 0; Indels 0; Gaps 0;
Matches 123; Conservative 0; MisMatches 0; ID 1 GKDFOQPETKICVGCPRDPTNSPELEBTLTTIKLNAAENNATFYFKIDNVKARQVV 60
QY 253 GKDFOQPETKICVGCPRDPTNSPELEBTLTTIKLNAAENNATFYFKIDNVKARQVV 312
Db 253 GKDFOQPETKICVGCPRDPTNSPELEBTLTTIKLNAAENNATFYFKIDNVKARQVV 312
CC Sequence 644 AA;

Query Match 100.0%; Score 660; DB 5; Length 644;
Best Local Similarity 100.0%; Pred. No. 2.3e-65; Mismatches 0; Indels 0; Gaps 0;
Matches 123; Conservative 0; MisMatches 0; ID 1 GKDFOQPETKICVGCPRDPTNSPELEBTLTTIKLNAAENNATFYFKIDNVKARQVV 60
QY 253 GKDFOQPETKICVGCPRDPTNSPELEBTLTTIKLNAAENNATFYFKIDNVKARQVV 312
Db 253 GKDFOQPETKICVGCPRDPTNSPELEBTLTTIKLNAAENNATFYFKIDNVKARQVV 312
CC Sequence 644 AA;

Query Match 100.0%; Score 660; DB 5; Length 644;
Best Local Similarity 100.0%; Pred. No. 2.3e-65; Mismatches 0; Indels 0; Gaps 0;
Matches 123; Conservative 0; MisMatches 0; ID 1 GKDFOQPETKICVGCPRDPTNSPELEBTLTTIKLNAAENNATFYFKIDNVKARQVV 60
QY 253 GKDFOQPETKICVGCPRDPTNSPELEBTLTTIKLNAAENNATFYFKIDNVKARQVV 312
Db 253 GKDFOQPETKICVGCPRDPTNSPELEBTLTTIKLNAAENNATFYFKIDNVKARQVV 312
CC Sequence 644 AA;

Query Match 100.0%; Score 660; DB 5; Length 644;
Best Local Similarity 100.0%; Pred. No. 2.3e-65; Mismatches 0; Indels 0; Gaps 0;
Matches 123; Conservative 0; MisMatches 0; ID 1 GKDFOQPETKICVGCPRDPTNSPELEBTLTTIKLNAAENNATFYFKIDNVKARQVV 60
QY 253 GKDFOQPETKICVGCPRDPTNSPELEBTLTTIKLNAAENNATFYFKIDNVKARQVV 312
Db 253 GKDFOQPETKICVGCPRDPTNSPELEBTLTTIKLNAAENNATFYFKIDNVKARQVV 312
CC Sequence 644 AA;

Query Match 100.0%; Score 660; DB 5; Length 644;
Best Local Similarity 100.0%; Pred. No. 2.3e-65; Mismatches 0; Indels 0; Gaps 0;
Matches 123; Conservative 0; MisMatches 0; ID 1 GKDFOQPETKICVGCPRDPTNSPELEBTLTTIKLNAAENNATFYFKIDNVKARQVV 60
QY 253 GKDFOQPETKICVGCPRDPTNSPELEBTLTTIKLNAAENNATFYFKIDNVKARQVV 312
Db 253 GKDFOQPETKICVGCPRDPTNSPELEBTLTTIKLNAAENNATFYFKIDNVKARQVV 312
CC Sequence 644 AA;

Query Match 100.0%; Score 660; DB 5; Length 644;
Best Local Similarity 100.0%; Pred. No. 2.3e-65; Mismatches 0; Indels 0; Gaps 0;
Matches 123; Conservative 0; MisMatches 0; ID 1 GKDFOQPETKICVGCPRDPTNSPELEBTLTTIKLNAAENNATFYFKIDNVKARQVV 60
QY 253 GKDFOQPETKICVGCPRDPTNSPELEBTLTTIKLNAAENNATFYFKIDNVKARQVV 312
Db 253 GKDFOQPETKICVGCPRDPTNSPELEBTLTTIKLNAAENNATFYFKIDNVKARQVV 312
CC Sequence 644 AA;

Query Match 100.0%; Score 660; DB 5; Length 644;
Best Local Similarity 100.0%; Pred. No. 2.3e-65; Mismatches 0; Indels 0; Gaps 0;
Matches 123; Conservative 0; MisMatches 0; ID 1 GKDFOQPETKICVGCPRDPTNSPELEBTLTTIKLNAAENNATFYFKIDNVKARQVV 60
QY 253 GKDFOQPETKICVGCPRDPTNSPELEBTLTTIKLNAAENNATFYFKIDNVKARQVV 312
Db 253 GKDFOQPETKICVGCPRDPTNSPELEBTLTTIKLNAAENNATFYFKIDNVKARQVV 312
CC Sequence 644 AA;

Query Match 100.0%; Score 660; DB 5; Length 644;
Best Local Similarity 100.0%; Pred. No. 2.3e-65; Mismatches 0; Indels 0; Gaps 0;
Matches 123; Conservative 0; MisMatches 0; ID 1 GKDFOQPETKICVGCPRDPTNSPELEBTLTTIKLNAAENNATFYFKIDNVKARQVV 60
QY 253 GKDFOQPETKICVGCPRDPTNSPELEBTLTTIKLNAAENNATFYFKIDNVKARQVV 312
Db 253 GKDFOQPETKICVGCPRDPTNSPELEBTLTTIKLNAAENNATFYFKIDNVKARQVV 312
CC Sequence 644 AA;

XX Human G-protein coupled receptor related protein, GPCR related protein; NOV; cytosolic; cardiot; anti-arteriosclerotic; antiidiabetic; immunomodulator; anti-HIV; anorectic; antiasthmatic; haemostatic; anti-parkinsonian; neuroprotective; rootopic; gene therapy; vaccine; NOVX-associated disorder; cardiomyopathy; atherosclerosis; cancer;

diabetes; immune disorder; AIDS; obesity; asthma; haematopoietic disorder; Parkinson's disease; infection; multiple sclerosis; cancer-associated cachexia; wasting disorder; chronic disease; neurogenesis; cell proliferation; haemopoiesis; wound healing; angiogenesis; chromosome mapping; tissue typing; preventive medicine; pharmacogenomic.

XX OS Homo sapiens.

XX WO200299116-A2.

PD 12-DEC-2002.

XX PF 04-JUN-2002; 2002WO-US017428.

XX PR 04-JUN-2001; 2001US-0295607P.

PR 04-JUN-2001; 2001US-0295661P.

PR 06-JUN-2001; 2001US-0296104P.

PR 06-JUN-2001; 2001US-0296418P.

PR 14-JUN-2001; 2001US-0298285P.

PR 15-JUN-2001; 2001US-0298556P.

PR 21-JUN-2001; 2001US-029949P.

PR 26-JUN-2001; 2001US-0299949P.

PR 28-JUN-2001; 2001US-0300883P.

PR 13-AUG-2001; 2001US-031197P.

PR 27-AUG-2001; 2001US-0311507P.

PR 29-AUG-2001; 2001US-0315660P.

PR 14-SEP-2001; 2001US-032249P.

PR 17-SEP-2001; 2001US-0322706P.

PR 14-DEC-2001; 2001US-0341186P.

PR 28-FEB-2002; 2002US-036189P.

PR 12-MAR-2002; 2002US-0363673P.

PR 12-MAR-2002; 2002US-0363676P.

PR 03-JUN-2002; 2002US-0363676.

DR WPI; 2003-140627/13.

DR N-PSDB; ACD03654.

XX (CURA-) CURAGEN CORP.

PT New NOVX polypeptides and nucleic acids, useful for preventing or

treating NOVX-associated disorders, e.g. cancer, cardiomopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or

pharmacogenomics.

XX Claim 1: Page 148; 332pp; English.

XX The invention describes an isolated polypeptide (I) comprising any of 27

CC 118-961 residue amino acid sequences, given in the specification, a CC mature form of them, a sequence that is at least 95 % identical to them, CC or a sequence having one or more conservative substitutions in them. The CC polypeptide is useful in manufacturing a medicament for treating a CC syndrome associated with a human disease selected from a pathology CC associated with the polypeptide. The NOVX polypeptides, polymucleotides CC and antibodies are useful in treating or preventing NOVX-associated CC disorders, e.g. cardiomopathy, atherosclerosis, cancer, diabetes, immune CC disorders, AIDS, obesity, asthma, haematopoietic disorders, Parkinson's CC disease, Alzheimer's disease, infections, multiple sclerosis, cancer- CC associated cachexia, and other wasting disorders associated with chronic CC diseases. The nucleic acids and polypeptides may also be used as targets CC for the identification of small molecules that modulate or inhibit e.g. CC neurogenesis, cell differentiation, cell proliferation, haemopoiesis, CC wound healing and angiogenesis, in gene therapy, in generation of CC antibodies that bind immunospecifically to NOVX substances for use in CC therapeutic or diagnostic methods. The nucleic acids are further used as CC hybridisation probes, in chromosome mapping, tissue typing, preventive CC medicine, and pharmacogenomics. The polypeptides are also useful as CC

CC vaccines. This is the amino acid sequence of a novel human G-protein CC coupled receptor related protein NOV

XX SQ Sequence 644 AA;

Query Match 100.0%; Score 660; DB 6; Length 644;

Best Local Similarity 100.0%; Pred. No. 2.3e-55; Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKDFFQQPPRKICVGCPRDIPNTSPELBTLHTITKNAENNATYFKIDNTVKKARYQVV 60

Db 253 GKDFFQQPPRKICVGCPRDIPNTSPELBTLHTITKNAENNATYFKIDNTVKKARYQVV 312

QY 61 AGKXYFIDFVARETCSKESNEELTESCTRKLGQSLDCNAEVYYVWEKLYPTYNQCP 120

Db 313 AGKXYFIDFVARETCSKESNEELTESCTRKLGQSLDCNAEVYYVWEKLYPTYNQCP 372

RESULT 14

ABU99145

ID ABU99145 standard; protein; 644 AA.

XX

AC ABU99145;

XX

DT 01-AUG-2003 (first entry)

XX Novel human GPCR related protein NOV12C.

DE ABU99145

XX

XW Human; G-protein coupled receptor related protein;

XW immunomodulator; anti-HIV; anorectic; antiastmatic; haemostatic;

XW anti-parkinsonian; neuroprotective; nootropic; cardiotonic; antiabetic;

XW XW antiparkinsonian; cardiotonic; atherosclerosis; cancer;

XW diabetes; immune disorder; AIDS; obesity; asthma;

XW haematopoietic disorder; Parkinson's disease; Alzheimer's disease;

XW infection; multiple sclerosis; cancer-associated cachexia;

XW wasting disorder; Chronic disease; neurogenesis; cell differentiation;

XW cell proliferation; haemopoiesis; wound healing; angiogenesis;

XW chromosome mapping; tissue typing; preventive medicine; pharmacogenomic.

XX Homo sapiens.

OS XX

PN PN WO200299116-A2.

XX PD 12-DEC-2002.

XX PP 04-JUN-2002; 2002WO-US017428.

XX PR 04-JUN-2001; 2001US-0295607P.

PR 04-JUN-2001; 2001US-0295661P.

PR 06-JUN-2001; 2001US-0296404P.

PR 06-JUN-2001; 2001US-029648P.

PR 14-JUN-2001; 2001US-0298285P.

PR 15-JUN-2001; 2001US-0298556P.

PR 26-JUN-2001; 2001US-0300883P.

PR 28-JUN-2001; 2001US-031197P.

PR 13-AUG-2001; 2001US-031197P.

PR 27-AUG-2001; 2001US-0315071P.

PR 29-AUG-2001; 2001US-0315660P.

PR 14-SEP-2001; 2001US-0322706P.

PR 26-JUN-2001; 2001US-0300883P.

PR 28-JUN-2001; 2001US-0301550P.

PR 14-DEC-2001; 2001US-0341186P.

PR 14-DEC-2002; 2002WO-US017428.

(CURA-) CURAGEN CORP.

PA

XX Anderson DW, Baumgartner JC, Boldog FL, Casman SJ, Edinger SR;
 PI Gangolli EA, Gerlach VL, Guo X, Hjalt T, Kekuda R, Li L;
 PI Macdougall JR, Malanykaran UM, Millet I, Padigaru M, Patturajan M;
 PI Pena CEA, Rastelli L, Shimkets RA, Stone DJ, Spytel KA, Vernet CAM;
 PI Voss EZ, Zerhusen BD;

XX WPI; 2003-140627/1.3.
 DR N-PSDB; ACD03649.

XX New NOVX polypeptides and nucleic acids, useful for preventing or
 treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
 atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
 pharmacogenomics.

XX Claim 1; Page 144-145; 33pp; English.

CC The invention describes an isolated polypeptide (I) comprising any of 27
 CC 118-961 residue amino acid sequences, given in the specification, a
 CC mature form of them, a sequence that is at least 95 % identical to them,
 CC or a sequence having one or more conservative substitutions in them. The
 CC polypeptide is useful in manufacturing a medicament for treating a
 CC syndrome associated with a human disease selected from a pathology
 CC associated with the polypeptide. The NOVX polypeptides, polynucleotides
 CC and antibodies are useful in treating or preventing NOVX-associated
 CC disorders, e.g. cardiomyopathy, atherosclerosis, cancer, diabetes, immune
 CC disorders, AIDS, obesity, asthma, haemopoietic disorders, Parkinson's
 CC disease, Alzheimer's disease, infections, multiple sclerosis, cancer-
 CC associated cachexia, and other wasting disorders associated with chronic
 CC diseases. The nucleic acids and polypeptides may also be used as targets
 CC for the identification of small molecules that modulate or inhibit e.g.,
 CC neurogenesis, cell proliferation, hematopoiesis,
 CC wound healing and angiogenesis, in gene therapy, in generation of
 CC antibodies that bind immunospecifically to NOVX substances for use in
 CC therapeutic or diagnostic methods. The nucleic acids are further used as
 CC hybridisation probes, in chromosome mapping, tissue typing, preventive
 CC medicine, and pharmacogenomics. The polypeptides are also useful as
 CC vaccines. This is the amino acid sequence of a novel human G-protein
 CC coupled receptor related protein NOV
 XX Sequence 644 AA;

Query Match 100.0%; Score 660; DB 6; Length 644;
 Best Local Similarity 100.0%; Pred. No. 2.3e-65; Indels 0; Gaps 0;
 Matches 123; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 GKDVFQPPTKICVGCPDRDPTNSPELEETLTTITKNAENNATYFKIDNVKKARVQVY 60
 Db 253 GKDVFQPPTKICVGCPDRDPTNSPELEETLTTITKNAENNATYFKIDNVKKARVQVY 312

Qy 61 AGKRYFIDFVARETTCSKESNEELTESCTKLQGSLDCNAEVVYYPWEEKIYPTVNQCP 120
 Db 313 AGKRYFIDFVARETTCSKESNEELTESCTKLQGSLDCNAEVVYYPWEEKIYPTVNQCP 372

Qy 121 LGM 123
 Db 373 LGM 375

RESULT 15
 AAB37447 standard; protein; 122 AA.
 ID AAB37447
 AC AAB37447;
 XX DT 21-FEB-2001 (first entry)
 DE Human kininogen D3.
 XX Enzyme; legumain; endopeptidase; cystatin; human; kininogen.
 XX Homo sapiens.
 XX

PN HC0300064945-A1.
 XX PD 02-NOV-2000.
 XX PF 20-APR-2000; 2000WO-GB0001571.
 XX PR 22-APR-1999; 99GB-00009133.
 XX PA (BABR-) BABRAHAM INST.
 XX PI Abrahamson M, Barrett AJ;
 XX DR 2000-687316/67.
 PT PT Inhibition of mammalian legumain or legumain-related endopeptidase by
 PT cystatin involves interaction with second papain-non-reactive site of
 PT cystatin.
 PS Disclosure; Fig 4; 45pp; English.
 XX The present invention relates to inhibition of the enzymatic activity of
 CC legumain or a legumain-related endopeptidase by cystatin. The inhibition
 CC involves an interaction between legumain and a papain-non-reactive site
 CC of cystatin. Legumain (EC 3.4.22.34) is a cysteine endopeptidase, and
 CC performs a protein-processing function. The present sequence is human
 CC kininogen D3, which was used in the present invention. Kininogen is a
 CC type 3 cystatin
 XX Sequence 122 AA;

Query Match 95.2%; Score 628; DB 3; Length 122;
 Best Local Similarity 100.0%; Pred. No. 9.5e-63;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPIKICVGCPDRDPTNSPELEETLTTITKNAENNATYFKIDNVKKARVQVACKYF 66
 Db 1 PPPIKICVGCPDRDPTNSPELEETLTTITKNAENNATYFKIDNVKKARVQVACKYF 60

Qy 67 IDFVARETICSKESENELTESCTKLQGSLDCNAEVVYYPWEEKIYPTVNQCP 123
 Db 61 IDFVARETICSKESENELTESCTKLQGSLDCNAEVVYYPWEEKIYPTVNQCP 117

Search completed: September 24, 2004, 14:08:37
 Job time : 52.692 secs

Result No.	Score	Query	Match	Length	DB	ID	Description
1	660	BLOSUM62	644	1	KNG_HUMAN	P01042	homo sapien
2	477	GapD 10.0 , Gapext 0.5	436	1	KNL1_BOVIN	P01046	bos taurus
3	477	Searched: 141681 seqs, 52070155 residues	621	1	KNH1_BOVIN	P01044	bos taurus
4	450	Total number of hits satisfying chosen parameters: 141681	434	1	KNL2_BOVIN	P01047	bos taurus
5	450	Minimum DB seq length: 0	619	1	KNH2_BOVIN	P01045	bos taurus
6	430	Maximum DB seq length: 200000000	661	1	KNG_MOUSE	Q08777	mus musculus
7	426	Post-processing: Minimum Match 0%	639	1	KNG RAT	P08834	rattus norvegicus
8	409	Maximum Match 100%	620	1	KNT2 RAT	P08932	rattus norvegicus
9	401	Lasting first 45 summaries	430	1	KNT1 RAT	P01048	rattus norvegicus
10	175	Database : iSwissProt_42.4*	265	1	CYTP_MOUSE	Q89988	mus musculus
11	165	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	251	1	CYTF_HUMAN	Q76196	homo sapien
12	138	Total number of hits satisfying chosen parameters: 141681	210	1	CYTC_BOVIN	Q15228	homo sapien
13	136	Minimum DB seq length: 0	148	1	CYTC_BOVIN	P01035	bos taurus
14	132	Maximum DB seq length: 200000000	146	1	CYTC_BOVIN	P14941	rattus norvegicus
15	132	Post-processing: Minimum Match 0%	202	1	CYTC_SAISC	P21460	mus musculus
16	130	Maximum Match 100%	201	1	CYTC RAT	Q9cpX9	rattus norvegicus
17	129	Lasting first 45 summaries	196	1	CYTC_MOUSE	Q9ucm5	homo sapien
18	129	Database : iSwissProt_42.4*	196	1	FETB_HUMAN	P01034	homo sapien
19	129	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	196	1	CYT_ESTAR	P09228	homo sapien
20	128	Total number of hits satisfying chosen parameters: 141681	111	1	CYT_HUMAN	Q97882	oryctolagus cuniculus
21	127	Minimum DB seq length: 0	146	1	CYT_RABIT	P81061	coturnix coqui
22	125	Maximum DB seq length: 200000000	141	1	CYT_COTUA	P01038	gallus gallus
23	124	Post-processing: Minimum Match 0%	148	1	CYT_CHICK	Q9pcf1	mus musculus
24	122	Maximum Match 100%	116	1	CYT_CHICK	P31277	sarcophaga
25	118	Lasting first 45 summaries	139	1	CYT_SARPE	P19133	rattus norvegicus
26	118	Database : iSwissProt_42.4*	180	1	CYT_RAT	P01037	homo sapien
27	113	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	175	1	CYT_N_HUMAN	P01036	homo sapien
28	113	Total number of hits satisfying chosen parameters: 141681	171	1	CYT_RABBIT	Q98967	oncorhynchus tshawytscha
29	109	Minimum DB seq length: 0	166	1	CYT_COTUA	P35481	cyprius carpio
30	109	Maximum DB seq length: 200000000	141	1	CYT_ONCVO	Q91195	oncorhynchus tshawytscha
31	108	Lasting first 45 summaries	164	1	CYT_ONCVO	P22085	onchocerca
32	108	Database : iSwissProt_42.4*	129	1	CYT_ONCVO	Q84269	mus musculus
33	106	Post-processing: Minimum Match 0%	161	1	CST1_HUMAN	Q91114	homo sapien
					CST2_MOUSE	P22766	mus musculus
					CST12_HUMAN	P21112	homo sapien
					CST18_MOUSE	P29699	mus musculus
					CYT_NAIA	P81714	zea mays (tm)
					CYT_MAJAT	P31726	zea mays (tm)
					CYT_HUMAN	P28325	homo sapien
					A2HS_RAT	P24090	rattus norvegicus
					CST8_RAT	OS88969	rattus norvegicus

ALIGNMENTS

RESULT 1							
KNG_HUMAN	ID	KNG_HUMAN	STANDARD;	PRT;	644 AA.		
	AC	P01042; P01043;	DT	21-JUL-1986 (Rel. 01, Created)			
			DT	01-FEB-1996 (Rel. 33, Last sequence update)			
			DT	10-OCT-2003 (Rel. 42, Last annotation update)			
			DE	Kininogen precursor (Alpha-2-thiol proteinase inhibitor)	[Contains:		
				KNG.			
			GN	Homo sapiens (Human).			
				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
			OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
			OX	NCBI_TAXID=9606;			
	RN	[1]	SEQUENCE FROM N.A. (ISOFORMS HNW AND LMW).				
	RP	SEQUENCE FROM N.A. (ISOFORMS HNW AND LMW).	RC	Tissue=Liver; MEDLINE=85234582; PubMed=2989293;			
	RX		RA	Takagaki Y., Kitamura N., Nakanishi S.;			
	RT	"Cloning and sequence analysis of cDNAs for human high molecular weight prekininogens."	RT	"Cloning and sequence analysis of cDNAs for human high molecular weight prekininogens."			
	RT	weight and low molecular weight prekininogens."	RT	weight and low molecular weight prekininogens."			
	RL	J. Biol. Chem. 260:8661-8669 (1985).	RL	J. Biol. Chem. 260:8610-8617 (1985).			
	RN		RN				
	RP	SEQUENCE OF 1-401 FROM N.A.	RP	SEQUENCE OF 1-401 FROM N.A.			
	RX	MEDLINE=85234583; PubMed=2989294;	RX	MEDLINE=85234583; PubMed=2989294;			
	RA	Onikubo T., Kurachi K., Takasawa T., Shiokawa H., Sasaki M., Miyata T.,	RA	Onikubo T., Kurachi K., Takasawa T., Shiokawa H., Sasaki M., Miyata T.,			
	RA	Nakanishi S.;	RA	Nakanishi S.;			
	RT	"Structural organization of the human kininogen gene and a model for its evolution."	RT	"Structural organization of the human kininogen gene and a model for its evolution."			
	RT	its identity with low molecular weight kininogen."	RT	its identity with low molecular weight kininogen."			
	RT	J. Biol. Chem. 260:8610-8617 (1985).	RT	J. Biol. Chem. 260:8610-8617 (1985).			
	RN		RN				
	RP	SEQUENCE OF 379-644.	RP	SEQUENCE OF 379-644.			
	RX	MEDLINE=86010270; PubMed=4054110;	RX	MEDLINE=86010270; PubMed=4054110;			
	PN	Lortspeich F., Kellermann J., Henschien A., Poersch B.,	PN	Lortspeich F., Kellermann J., Henschien A., Poersch B.,			
	RN	"The amino acid sequence of the light chain of human high-molecular-mass kininogen."	RN	"The amino acid sequence of the light chain of human high-molecular-mass kininogen."			
	RL	Eur. J. Biochem. 152:307-314 (1985).	RL	Eur. J. Biochem. 152:307-314 (1985).			
	RN		RN				
	RP	SEQUENCE OF 381-389.	RP	SEQUENCE OF 381-389.			
	RX	MEDLINE=90255622; PubMed=4952632;	RX	MEDLINE=90255622; PubMed=4952632;			
	RA	Pierce J.V.;	RA	Pierce J.V.;			
	RT	"Structural features of plasma kinins and kininogens."	RT	"Structural features of plasma kinins and kininogens."			
	RL	Proc. Natl. Acad. Sci. USA 75:52-57 (1978).	RL	Proc. Natl. Acad. Sci. USA 75:52-57 (1978).			
	RN		RN				
	[6]						
	RP	DISULFIDE BONDS.	RP	DISULFIDE BONDS.			
	RA	Sueyoshi T., Miyata T., Kato H., Iwanaga S.;	RA	Sueyoshi T., Miyata T., Kato H., Iwanaga S.;			
	RT	"Disulfide bonds in bovine HMW kininogens."	RT	"Disulfide bonds in bovine HMW kininogens."			

Seikatoku 56 :808-808 (1984).
 [7] RN GO; GO_0030147; P:natriuresis; NAS.
 CARBOHYDRATE-LINKAGE SITE ASN-294.
 RP DR GO; GO_0006539; P:smooth muscle contraction; NAS.
 RX DR Inter-PO; IPR000010; Cystatin.
 RA DR Pfam; PF00031; Cystatin_3.
 RT DR PRINTS; SM00043; CY_3.
 RT DR PROSITE; PS00287; CYSTATIN_2.
 RT Glycoprotein; Plasma; Repeat; Thiol protease inhibitor; Vasodilator;
 KW Bradykinin; Blood coagulation; Inflammatory response; Signal;
 CC KW Alternative splicing; Pyrrolidone carboxylic acid.
 CC FT SIGNAL 1 18
 CC FT CHAIN 19 644 KININOGEN.
 CC FT CHAIN 19 380 KININOGEN HEAVY CHAIN.
 CC FT PEPTIDE 381 389 BRADYKININ.
 CC FT CHAIN 390 644 KININOGEN LIGHT CHAIN.
 CC FT DOMAIN 19 136 CYSTATIN-LIKE 1.
 CC FT DOMAIN 137 258 CYSTATIN-LIKE 2.
 CC FT DOMAIN 259 380 CYSTATIN-LIKE 3.
 CC FT DOMAIN 420 510 HIS-RICH (ASSOCIATED WITH CLOTTING ACTIVITY).
 CC FT REPEAT 420 449 PYRROLIDONE CARBOXYLIC ACID.
 CC FT REPEAT 450 479 PYRROLIDONE CARBOXYLIC ACID.
 CC FT REPEAT 480 510 PYRROLIDONE CARBOXYLIC ACID.
 CC FT MOD_RES 19 19 PYRROLIDONE CARBOXYLIC ACID.
 CC FT DISULFID 28 614 INTERCHAIN.
 CC FT DISULFID 83 94
 CC FT DISULFID 107 126
 CC FT DISULFID 142 148
 CC FT DISULFID 206 218
 CC FT DISULFID 229 248
 CC FT DISULFID 264 284
 CC FT DISULFID 328 340
 CC FT DISULFID 351 370
 CC FT CARBOHYD 48 48 N-LINKED (GLCNAC, .) (POTENTIAL).
 CC FT CARBOHYD 169 169 N-LINKED (GLCNAC, .) (POTENTIAL).
 CC FT CARBOHYD 205 205 N-LINKED (GLCNAC, .) (POTENTIAL).
 CC FT CARBOHYD 294 294 N-LINKED (GLCNAC, .).
 CC FT CARBOHYD 401 401 O-LINKED.
 CC FT CARBOHYD 533 533 O-LINKED.
 CC FT CARBOHYD 542 542 O-LINKED.
 CC FT CARBOHYD 546 546 O-LINKED.
 CC FT CARBOHYD 557 557 O-LINKED.
 CC FT CARBOHYD 571 571 O-LINKED.
 CC FT CARBOHYD 577 577 O-LINKED.
 CC FT CARBOHYD 593 593 O-LINKED.
 CC FT CARBOHYD 628 628 O-LINKED.
 CC FT VARSPLIC 402 427 VSPPHMSMAPQDEERDSGKXEQGHTR -> SHLRSCEYKGR PPKAGAPASEEVs (in isoform LMW). /FTId=ISP_001261.
 CC FT VARSPLIC 428 644 Missing (In isoform LMW). /FTId=ISP_001262.
 CC FT CONFLICT 593 593 T -> I (IN REF_1). CRC64;
 CC SQ SEQUENCE 644 AA; 71945 MW;

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Query Match 100.0% ; Pred. No. 2e-55 ; Length 644 ;
 Best Local Similarity 100.0% ;
 Matches 123 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

QY 1 GKDFFQVPPTKIKCVCGRDPDIPTNSPELBTLTHITKLNAAENNATFYKIDNVKKGARVQVV 60
 Db 253 GKDFFQVPPTKIKCVCGRDPDIPTNSPELBTLTHITKLNAAENNATFYKIDNVKKGARVQVV 312

QY 61 AGKCKYFDIFDVARETTCSKESNSELTESETKLKGOSIDCNAEYYYYWEKXIIYPTVNQCP 120
 Db 313 AGKCKYFDIFDVARETTCSKESNSELTESETKLKGOSIDCNAEYYYYWEKXIIYPTVNQCP 372

QY 121 LGM 123
 Db 373 LGM 375

RESULT 2

FT	MOD_FBS	1.9	19	PYRROLIDONE CARBOXYLIC ACID.
FT	CARBHYD	87	87	N-LINKED (GLCNAC. .).
FT	CARBHYD	136	136	O-LINKED (PARTIAL. .).
FT	CARBHYD	168	168	N-LINKED (GLCNAC. .) (OR 169).
FT	CARBHYD	197	197	N-LINKED (GLCNAC. .) (PARTIAL).
FT	CARBHYD	204	204	N-LINKED (GLCNAC. .).
FT	DISUFLID	27	406	INTERCHAIN.
FT	DISUFLID	82	93	
FT	DISUFLID	106	125	
FT	DISUFLID	141	144	
FT	DISUFLID	205	217	
FT	DISUFLID	228	247	
FT	DISUFLID	263	266	
FT	DISUFLID	327	339	
FT	DISUFLID	350	369	
FT	CONFFLICT	295	295	A -> T (IN REF. 1; CAA23709).
SEQUENCE	436 AA;	48427 MW;	F01F7EB814BC6C CRC64;	
Query Match	72.3%	Score 477;	DB 1;	Length 436;
Best Local Similarity	71.3%;	Pred. No. 3.6e-38;		
Matches	87;	Conservative	14;	Mismatches 0;
Matches	87;	Indels	0;	Gaps 0;
Qy	2 KDFVQOPTKIVCGPDPINSPLEETLTITKLNAENNATTFKIDMVKKARYQVVA	61		
Db	253 KDFVQOPTKIVCGPDPINSPLEETLTITKLNAENNATTFKIDMVKKARYQVVA	312		
Qy	62 GKKYFIDFVARETTSKESNEELTSCETKLGQSLDCNAEYYYYPWERKLYPTVNQPL	121		
Db	313 GLKYSVIFVARETTSKGSNEELTSCEINHGQLHCDANVYVPPWEEKVYPTVNQPL	372		
RESULT 3	KNH1_BOVIN STANDARD; PRT; 621 AA.			
ID	KNH1_BOVIN			
AC	P01044;			
DT	21-JUL-1986 (Rel. 01; Created)			
DT	21-JUL-1986 (Rel. 01; Last sequence update)			
DT	28-FEB-2003 (Rel. 41; Last annotation update)			
DE	Kininogen, HMW I precursor (Thiol proteinase			
DR	Rabbitkinin].			
OS	Bos taurus (Bovine).			
OC	Kitamura, N.; Takagaki, Y.; Furuto, S.; Tanaka, T.; Nawa, H., Nakanishi, S.; Mammalia; Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi; Bovidae; Bovinae; Bos.			
OC	NCBI_TaxID=9913;			
RN	[1] —			
RN	SEQUENCE FROM N.A.			
MEDLINE=83117859; PubMed=6572010;				
NAME=KININOGEN I.				
PRIMARY STRUCTURE OF bovine liver low molecular weight kininogen precursors and their two mRNAs";				
Proc. Natl. Acad. Sci. U.S.A. 80:90-94 (1983).				
SEQUENCE OF 19-378.				
MEDLINE=87137530; PubMed=3546295;				
Sueyoshi T.; Miyata T.; Hashimoto N.; Kato H.; Hayashida H., Miyata T.; Iwamoto S.;				
"Bovine high molecular weight kininogen. The amino acid sequence, positions of carbohydrate chains and disulfide bridges in the heavy chain portion."				
J. Biol. Chem. 262:2768-2779 (1987).				
-!- FUNCTION: (1) Kininogens are inhibitors of thiol proteases; (2) LMW-kininogen inhibits the aggregation of thrombocytes; (3) the active peptide kallidin that is released from HMW-kininogen shows a variety of physiological effects: (3A) influence in smooth muscle contraction; (3B) induction of hypertension, (3C) natriuresis and diuresis (kidney).				
-!- SUBCELLULAR LOCATION: Extracellular.				
-!- ALTERNATIVE PRODUCTS:				
Event=Alternative splicing; Named isoforms=2;				
Name=LHM I;				
Isoid=PO1046-1; Sequence=Displayed;				
Name=HMW I;				
Isoid=PO1044-1; Sequence=External;				
-!- TISSUE/SPECIFICITY: Plasma.				
-!- PTM: Bradykinin is released from kininogen by plasma kallikrein.				
-!- MISCELLANEOUS: LMW-kininogen is in contrast to HMW-kininogen not involved in blood clotting.				
-!- SIMILARITY: Contains 3 cystatin-like domains.				
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EMBL: V00426; PIR: V00426; PIR: A01283; KGBO1; InterPro: IPR00010; Cystatin; SMART: SM00043; CYT, PROS1; PS00004; CYT, PROS1; PS0287; Cystatin; Glycoprotein; Plasma; Repeat; vascillator; Alternative splicing; Thiol protease inhibitor; Bradykinin; Signal; Pyrrolidone carboxylic acid.				
CHAIN SIGNAL 1 18	KININOGEN, LMW I.			
CHAIN 19 436	HEAVY CHAIN.			
CHAIN 19 378	BRADYKININ.			
PEPTIDE 388	LIGHT CHAIN.			
CHAIN 389 436	"Studies on the structure of bovine kininogen: cleavages of disulfide bonds and of methionyl bonds in kininogen-II."			
DOMAIN 136 257	J. Biol. Chem. 262:2768-2779 (1987).			
DOMAIN 258 378	RN [4]			

SEQUENCE OF 458-498.
MEDLINE=75170265; PubMed=1169237;
Han Y.N., Komiya M., Iwanaga S.; Suzuki T.;
Studies on the primary structure of bovine high-molecular-weight
kininogen. Amino acid sequence of a fragment ('histidine-rich
peptide') released by plasma kallikrein.;
J. Biochem. 77:55-68(1975).
-!- FUNCTION: (1) Kininogens are inhibitors of thiol proteases; (2)
HMW-kininogen play an important role in blood coagulation by
helping to position optimally prekallikrein and Factor XI next to
factor XII; (3) HMW-kininogen inhibits the thrombin- and plasmin-
induced aggregation of thrombocytes; (4) the active peptide
bradykinin that is released from HMW-kininogen shows a variety of
physiological effects: (4A) influence in smooth muscle
contraction, (4B) induction of hypertension, (4C) natriuresis and
diuresis, (4D) decrease in blood glucose level, (4E) it is a
mediator of inflammation and causes (4E) increase in vascular
permeability, (4B2) stimulation of nociceptors (4F) release of
other mediators of inflammation (e.g. prostaglandins), (4F) it has
a cardioprotective effect (directly via bradykinin action,
indirectly via endothelin-derived relaxing factor action).
-!- SUBCELLULAR LOCATION: Extracellular.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=HMW I;
IsoID=P01044-1; Sequence=Displayed;
Name=HMW I;
IsoID=P01046-1; Sequence=External;
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- PTN: Bradykinin is released from kininogen by plasma kallikrein.
CC -!- SIMILARITY: Contains 3 cystatin-like domains.
CC -!- This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
CC -!- EMBL; PIR; A01281; KGBOH1;
DR PIR; A01281; KGBOH1;
DR InterPro; IPR000010; Cystatin.
DR InterPro; IPR002395; Kininogen.
DR Pfam; PF00031; Cystatin; 3.
DR PRINTS; PR00334; KININOGEN.
DR SMART; SM00043; CY_3.
DR PROSITE; PS00287; CYSTATIN; 2.
DR Glycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing;
KW Thiol protease inhibitor; Bradykinin; Blood coagulation;
PT SIGNAL 1 PROBABLE.
PT CHAIN 19 621 18
FT PEPTIDE 19 378 388
FT CHAIN 19 389 621
FT DOMAIN 19 135 135
FT DOMAIN 136 257 258
FT DOMAIN 258 378 378
FT NOD_RES 19 19 19
FT CARBOHYD 87 87 87
FT CARBOHYD 136 136 136
FT CARBOHYD 168 168 168
FT CARBOHYD 197 197 197
FT DISULFID 204 204 204
FT DISULFID 27 591 591
FT DISULFID 82 93 93
FT DISULFID 106 125 125
FT DISULFID 141 144 144
FT DISULFID 205 217 217
FT DISULFID 228 247 247
FT DISULFID 263 266 266
FT DISULFID 327 339 339

SEQUENCE OF 350-369.
MEDLINE=75170265; PubMed=1169237;
SQ SEQUENCE 621 AA; 68890 MW; D16850BEBE3C55CD CRC64;
Query Match 72.3%; Score 477; DB 1; Length 621;
Best Local Similarity 71.9%; Pred. No. 5.4e-38;
Matches 87; Conservative 14; Mismatches 20; Indels 0; Gaps 0;
-!- TISSUE SPECIFICITY: Plasma.
CC -!- PTN: Bradykinin is released from kininogen by plasma kallikrein.
CC -!- SIMILARITY: Contains 3 cystatin-like domains.

SEQUENCE OF 369-373.
MEDLINE=75170265; PubMed=1169237;
SQ SEQUENCE 373 AA; 68890 MW; D16850BEBE3C55CD CRC64;
Query Match 72.3%; Score 477; DB 1; Length 621;
Best Local Similarity 71.9%; Pred. No. 5.4e-38;
Matches 87; Conservative 14; Mismatches 20; Indels 0; Gaps 0;
-!- TISSUE SPECIFICITY: Plasma.
CC -!- PTN: Bradykinin is released from kininogen by plasma kallikrein.
CC -!- SIMILARITY: Contains 3 cystatin-like domains.

SEQUENCE OF 373-378.
MEDLINE=75170265; PubMed=1169237;
SQ SEQUENCE 378 AA; 68890 MW; D16850BEBE3C55CD CRC64;
Query Match 72.3%; Score 477; DB 1; Length 621;
Best Local Similarity 71.9%; Pred. No. 5.4e-38;
Matches 87; Conservative 14; Mismatches 20; Indels 0; Gaps 0;
-!- TISSUE SPECIFICITY: Plasma.
CC -!- PTN: Bradykinin is released from kininogen by plasma kallikrein.
CC -!- SIMILARITY: Contains 3 cystatin-like domains.

SEQUENCE OF 378-393.
MEDLINE=75170265; PubMed=1169237;
SQ SEQUENCE 393 AA; 68890 MW; D16850BEBE3C55CD CRC64;
Query Match 72.3%; Score 477; DB 1; Length 621;
Best Local Similarity 71.9%; Pred. No. 5.4e-38;
Matches 87; Conservative 14; Mismatches 20; Indels 0; Gaps 0;
-!- TISSUE SPECIFICITY: Plasma.
CC -!- PTN: Bradykinin is released from kininogen by plasma kallikrein.
CC -!- SIMILARITY: Contains 3 cystatin-like domains.

SEQUENCE OF 393-434.
MEDLINE=75170265; PubMed=1169237;
SQ SEQUENCE 434 AA; 68890 MW; D16850BEBE3C55CD CRC64;
Query Match 72.3%; Score 477; DB 1; Length 621;
Best Local Similarity 71.9%; Pred. No. 5.4e-38;
Matches 87; Conservative 14; Mismatches 20; Indels 0; Gaps 0;
-!- TISSUE SPECIFICITY: Plasma.
CC -!- PTN: Bradykinin is released from kininogen by plasma kallikrein.
CC -!- SIMILARITY: Contains 3 cystatin-like domains.

SEQUENCE OF 434-458.
MEDLINE=75170265; PubMed=1169237;
SQ SEQUENCE 458 AA; 68890 MW; D16850BEBE3C55CD CRC64;
Query Match 72.3%; Score 477; DB 1; Length 621;
Best Local Similarity 71.9%; Pred. No. 5.4e-38;
Matches 87; Conservative 14; Mismatches 20; Indels 0; Gaps 0;
-!- TISSUE SPECIFICITY: Plasma.
CC -!- PTN: Bradykinin is released from kininogen by plasma kallikrein.
CC -!- SIMILARITY: Contains 3 cystatin-like domains.

SEQUENCE OF 458-498.
MEDLINE=75170265; PubMed=1169237;
Han Y.N., Komiya M., Iwanaga S.; Suzuki T.;
Studies on the primary structure of bovine high-molecular-weight
kininogen. Amino acid sequence of a fragment ('histidine-rich
peptide') released by plasma kallikrein.;
J. Biochem. 77:55-68(1975).
-!- FUNCTION: (1) Kininogens are inhibitors of thiol proteases; (2)
HMW-kininogen play an important role in blood coagulation by
helping to position optimally prekallikrein and Factor XI next to
factor XII; (3) HMW-kininogen inhibits the thrombin- and plasmin-
induced aggregation of thrombocytes; (4) the active peptide
bradykinin that is released from HMW-kininogen shows a variety of
physiological effects: (4A) influence in smooth muscle
contraction, (4B) induction of hypertension, (4C) natriuresis and
diuresis, (4D) decrease in blood glucose level, (4E) it is a
mediator of inflammation and causes (4E) increase in vascular
permeability, (4B2) stimulation of nociceptors (4F) release of
other mediators of inflammation (e.g. prostaglandins), (4F) it has
a cardioprotective effect (directly via bradykinin action,
indirectly via endothelin-derived relaxing factor action).
-!- SUBCELLULAR LOCATION: Extracellular.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=HMW I;
IsoID=P01044-1; Sequence=Displayed;
Name=HMW I;
IsoID=P01046-1; Sequence=External;
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- PTN: Bradykinin is released from kininogen by plasma kallikrein.
CC -!- SIMILARITY: Contains 3 cystatin-like domains.
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or send an email to license@isb-sib.ch).
CC -!- EMBL; PIR; A01281; KGBOH1;
DR PIR; A01281; KGBOH1;
DR InterPro; IPR000010; Cystatin.
DR InterPro; IPR002395; Kininogen.
DR Pfam; PF00031; Cystatin; 3.
DR PRINTS; PR00334; KININOGEN.
DR SMART; SM00043; CY_3.
DR PROSITE; PS00287; CYSTATIN; 2.
DR Glycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing;
KW Thiol protease inhibitor; Bradykinin; Blood coagulation;
PT SIGNAL 1 PROBABLE.
PT CHAIN 19 621 18
FT PEPTIDE 19 378 388
FT CHAIN 19 389 621
FT DOMAIN 19 135 135
FT DOMAIN 136 257 258
FT DOMAIN 258 378 378
FT NOD_RES 19 19 19
FT CARBOHYD 87 87 87
FT CARBOHYD 136 136 136
FT CARBOHYD 168 168 168
FT CARBOHYD 197 197 197
FT DISULFID 204 204 204
FT DISULFID 27 591 591
FT DISULFID 82 93 93
FT DISULFID 106 125 125
FT DISULFID 141 144 144
FT DISULFID 205 217 217
FT DISULFID 228 247 247
FT DISULFID 263 266 266
FT DISULFID 327 339 339

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CC EMBL; V00427; CAA2370_1; -.
CC PIR; A01284; KGB012.
DR HSSP; P0108; IAP0.
DR InterPro; IPR00010; Cystatin.
DR Pfam; PF00031; cystatin; 3.
DR SMART; SM0003; CY; 3.
DR PROSITE; PS00287; CYSTATIN; 2.
DR Glycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing; Thiol protease inhibitor; Bradykinin; Signal; Pyroldidine carboxylic acid.
FT SIGNAL 1 18
FT CHAIN 19 434 KININOPEN, LMW II.
FT PEPTIDE 19 376 HEAVY CHAIN.
FT CHAIN 378 386 BRADYKININ.
FT DOMAIN 19 434 LIGHT CHAIN.
FT DOMAIN 136 256 CYSTATIN-LIKE 1.
FT DOMAIN 257 376 CYSTATIN-LIKE 2.
FT MOD_BES 19 19 PYRROLIDONE CARBOXYLIC ACID.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. .).
FT CARBOHYD 136 136 O-LINKED (PARTIAL).
FT CARBOHYD 168 168 N-LINKED (GLCNAC. .) (OR 169).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. .) (PARTIAL).
FT CARBOHYD 204 204 N-LINKED (GLCNAC. .).
FT CARBOHYD 280 280 N-LINKED (GLCNAC. .).
FT DISUFID 27 404 INTERCHAIN.
FT DISUFID 82 93
FT DISUFID 106 125
FT DISUFID 141 144
FT DISUFID 205 217
FT DISUFID 228 247
FT DISUFID 261 264
FT DISUFID 325 337
FT DISUFID 348 367
SQ SEQUENCE 434 AA; 48148 MW; 73A7079DE3E03430 CRC64;

Query Match 68.2%; Score 450; DB 1; Length 434;
Best Local Similarity 68.9%; Pred. No. 1.4e-35;
Matches 84; Conservative 14; Mismatches 22; Indels 2; Gaps 1;
SQ SEQUENCE 434 AA; 48148 MW; 73A7079DE3E03430 CRC64;

Qy 1 GKDFVQPPTKIVGCPDRDPTNSPELETTHTITKLNAAENNATFYKLDVNVKKARYQVY 60
Db 252 GEDFL-PPMVCGCERPKPDSPDDEAHNSTAKRNASHDGTFFYKCDTVKETQVY 309
Qy 61 AGKKYKIDFVARETTCSEKSNNEELTESCTKLGQSILDCAEVYVWKKLYPTVNCQP 120
Db 310 GGLKTSIVTFARRETTCSEKGSNNEELTKSCEINHGQILHCDANVYVPMWBKVZPTVNCCP 369
Qy 121 LG 122
Db 370 LG 371

CC MEDLINE=84014106; PubMed=6571699;
CC Kitamura N., Takagaki Y., Furuto S., Tanaka T., Nawa H., Nakanishi S.;
CC "A single gene for bovine high molecular weight kininogen and low molecular
CC weight kinogens"; Nature 305:545-549(1983).
DR [2].
RN SEQUENCE OF 19-376.
RX MEDLINE=8713730; PubMed=3546295;
RA Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H.,
RA Miyata T., Iwanaga S.; "Bovine high molecular weight kininogen. The amino acid sequence,
RT positions of carbohydrate chains and disulfide bridges in the heavy
chain portion.," J. Biol. Chem. 262:2768-2779(1987).
RN [3].
RN SEQUENCE OF 376-391.
RX MEDLINE=70180420; PubMed=4986212;
RA Kato H., Nagasawa S., Suzuki T.; "Studies on the structure of bovine kininogen: cleavages of disulfide
RT bonds and of methionyl bonds in kininogen-II.," J. Biochem. 67:313-323(1970).
RN [4].
RN SEQUENCE OF 377-455.
RX MEDLINE=76260155; PubMed=956151;
RA Han Y.N., Kato H., Iwanaga S., Suzuki T.; "Primary structure of plasma high-molecular-weight kininogen. The amino acid sequence of a glycopeptide portion (fragment 1)
RT following the C-terminus of the bradykinin moiety.," J. Biochem. 79:1201-1222(1976).
RN [5].
RN SEQUENCE OF 456-496.
RX MEDLINE=75170265; PubMed=1169237;
RA Han Y.N., Komiyama M., Iwanaga S., Suzuki T.; "Studies on the primary structure of bovine plasma kininogen. Amino acid sequence of a fragment ('histidine-rich
peptide') released by plasma kallikrein.," J. Biochem. 77:55-68(1975).
RN [-] FUNCTION: (1) Kininogen are inhibitors of thiol proteases; (2)
CC helping to position factor XI next to
CC optimally prekallikrein and factor XI next to
CC factor XII; (3) HMW-kininogen inhibits the thrombin- and plasmin-
CC induced aggregation of thrombocytes; (4) the active peptide
CC bradykinin that is released from HMW-kininogen shows a variety of
CC physiological effects: (4A) influence in smooth muscle
CC contraction, (4B) induction of hypotension, (4C) natriuresis and
CC diuresis, (4D) decrease in blood glucose level, (4E) it is a
CC mediator of inflammation and causes (4E1) increase in vascular
CC permeability, (4E2) stimulation of nociceptors (4E3) release of
CC other mediators of inflammation (e.g. prostaglandins), (4F) it has
CC a cardioprotective effect (directly via bradykinin action,
CC indirectly via endothelium-derived relaxing factor action).
RN [-] SUBCELLULAR LOCATION: Extracellular.
RN [-] ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=HMW III;
CC IsoId=P010405-1; Sequence=Displayed;
CC Name=LWV III;
CC IsoId=P01047-1; Sequence=External;
CC [-] TISSUE SPECIFICITY: Plasma;
CC [-] PTM: Bradykinin is released from kininogen by plasma kallikrein.
CC [-] SIMILARITY: Contains 3 cystatin-like domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC DR EMBL; V01492; CA24736.1;
DR FIR; A01282; KGBOH2.
DR HSSP; P01038; IAS0.

CC a cardioprotective effect (directly via bradykinin action, (5)
 CC indirectly via endothelium-derived relaxing factor action); (5)
 CC LMW-kininogen inhibits the aggregation of thrombocytes; (6) LMW
 CC kininogen is in contrast to HMW-kininogen not involved in blood
 CC clotting (BY similarity).
 CC !- SUBCELLULAR LOCATION: Secreted.
 CC !- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=HMW;
 CC IsoId=008677-1; Sequence=Displayed;
 CC
 CC TISoId=008677-2; Sequence=vSP_001263, VSP_001264;
 CC !- TISSUE SPECIFICITY: Plasma.
 CC !- PTM: Bradykinin is released from kininogen by plasma kallikrein.
 CC !- SIMILARITY: Contains 3 cystatin-like domains.
 CC
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 CC
 DR EMBL: DB4435; BAA19743.1; -;
 DR EMBL: DB4415; BAA19742.1; -;
 DR EMBL: AK005547; BAB24115.1; -;
 DR EMBL: BC018158; AAH18158.1; -;
 DR MGI: MG1:1097705; Xnkg.
 DR InterPro: IPR000110; Cystatin.
 DR InterPro: IPR002395; Kininogen.
 DR PRINTS: PR00031; cystatin_3.
 DR SMART: SM00443; CY_3.
 DR PROSITE: PS00281; CYSTATIN_1.
 KW Glycoprotein; Plasma; Repeate; Thiol protease inhibitor; Vasodilator;
 KW Bradykinin; Blood coagulation; Inflammatory response; Signal;
 KW Alternative splicing.
 SIGNAL 1 18
 FT CHAIN 19 661
 FT CHAIN 19 379
 FT CHAIN 380 388
 FT CHAIN 389 661
 FT DOMAIN 19 135
 FT DOMAIN 136 257
 FT DOMAIN 258 379
 FT DOMAIN 439 524
 FT DISULFID 28 631
 FT DISULFID 83 94
 FT DISULFID 107 125
 FT DISULFID 141 144
 FT DISULFID 205 217
 FT DISULFID 228 247
 FT DISULFID 263 266
 FT DISULFID 327 339
 FT DISULFID 350 369
 FT CARBOHYD 125 BY SIMILARITY.
 FT CARBOHYD 144 BY SIMILARITY.
 FT CARBOHYD 205 BY SIMILARITY.
 FT CARBOHYD 228 BY SIMILARITY.
 FT CARBOHYD 263 BY SIMILARITY.
 FT DISULFID 327 BY SIMILARITY.
 FT DISULFID 350 BY SIMILARITY.
 FT CARBOHYD 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 168 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 204 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 401 432 VSPPTIAREQDERAETQQCPTHGGMHLHQ -> RLRRA
 FT VARSPLIC 433 661 CEYKGRSLSKAGAEPAPERQAESSQVKQ (in isoform
 SQ SEQUENCE 661 AA; 73102 MW; Missing (in isoform LMW).
 FT /FTid=vSP_001263.
 FT /FTid=vSP_001264.
 FT VARSPLIC 433 661 Score 430; DB 1; Length 661;
 FT Best Local Similarity 65.2%; Pred. No. 1.8e-33;
 FT Matches 81; Conservative 65.9%; Pred. No. 1e-31; Indels 0; Gaps 0;
 FT Mismatches 11; Missmatches 31;

Db 252 GDLVLEALPKPQPGCPDPIDVPSPERKEVLGHISQIAQNAENDHPFPYKIDTVKQNSQV 311
 Qy 61 AGKKYFIDFVAEETTCSKESNBEITSCSETKLGQSLDCNAEVYTTWEEKLYPTVNCOP 120
 Db 312 AGTKYVIEIFIARETKCSKESNTELAEDCEIKHLGQSLDCNANVYMEPEWENKVPTVTCQA 371
 Qy 121 LGM 123
 Db 372 LDM 374

RESULT 7
 KNG_RAT STANDARD; PRT; 639 AA.
 ID KNG_RAT P08933; DT 01-NOV-1988 (Rel. 09, Created)
 AC P08934; DT 01-NOV-1988 (Rel. 09, Last sequence update)
 RA Kitagawa H., Kitamura N., Hayashita H., Miyata T., Nakanishi S.;
 DE "differing expression patterns and evolution of the rat kininogen
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Etheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OC NCBI_TaxID=10116;
 OX RN
 RP SEQUENCE FROM N.A. (ISOFORMS HMW AND LMW).
 MEDLINE=87137443; PubMed=10294068;
 RX RA
 Kitagawa H., Kitamura N., Hayashita H., Miyata T., Nakanishi S.;
 RT "differing expression patterns and evolution of the rat kininogen
 gene family";
 RT J. Biol. Chem. 262:2190-2198 (1987).
 RN RP SEQUENCE FROM N.A. (ISOFORM LMW).
 MEDLINE=86008264; PubMed=24130187;
 RX RA
 Furuta-Kato S., Matsumoto A., Kitamura N., Nakanishi S.;
 RT "Primary structures of the mRNAs encoding the rat precursors for
 bradykinin and T-kinin. Structural relationships of kininogens with
 RT major acute phase protein and alpha 1-cysteine proteinase
 RT inhibitor".
 RT J. Biol. Chem. 260:12054-12059 (1985).
 RN [3]
 RN SEQUENCE OF 1-65 FROM N.A.
 RP RC
 STRAIN=Buffalo;
 MEDLINE=87230580; PubMed=2439509;
 RX RA
 Fung W.-P., Schreiber G.;
 RT "Structure and expression of the genes for major acute phase alpha 1-
 RT protein (thiotrastin) and kininogen in the rat.";
 RT J. Biol. Chem. 262:9258-9308 (1987).
 RN [4]
 RN SEQUENCE OF 1-41 FROM N.A.
 RP RC
 STRAIN=Wistar; TISSUE=Liver;
 MEDLINE=87137465; PubMed=8118598;
 RX RA
 Kageyama R., Kitamura N., Ohkubo H., Nakanishi S.;
 RT "Utilization of homologous transcription initiation sites
 RT of rat K and T kininogen genes under inflammation condition.";
 RT J. Biol. Chem. 262:245-251 (1987).
 RL CC
 FUNCTION: (1) Kininogens are inhibitors of thiol proteases; (2)
 CC HMW-kininogen plays an important role in blood coagulation by
 CC helping to position optimally prekallikrein and factor XI next to
 CC factor XII; (3) HMW-kininogen inhibits the thrombin and plasmin-
 CC induced aggregation of thrombocytes; (4) the active peptide
 CC bradykinin that is released from HMW-kininogen shows a variety of
 CC physiological effects: (4A) influence in smooth muscle
 CC contraction, (4B) induction of hypotension, (4C) natriuresis and
 CC diuresis, (4D) decrease in blood glucose level, (4E) it is a
 CC mediator of inflammation and causes (4E1) increase in vascular
 CC permeability, (4E2) stimulation of nociceptors (4E3) release of
 CC other mediators of inflammation (e.g. prostaglandins), (4F) it has
 CC a cardioprotective effect (directly via bradykinin
 CC indirectly via endothelium-derived relaxing factor action); (5)
 CC LMW-kininogen inhibits the aggregation of thrombocytes; (6) LMW-
 CC kininogen is in contrast to HMW-kininogen not involved in blood

Query Match 1 GKDFVOPPTKICVGCPDRIPNSPLEBILTHIKNENNATPFKIDDNVKARVQV 60

CC	-!- clotting.	Best Local Similarity 65.0%; Pred. No. 4.1e-33;
CC	-!- SUBCELLULAR LOCATION: Secreted.	Matches 80; Conservative 14; Mismatches 29; Indels 0; Gaps 0;
CC	-!- ALTERNATIVE PRODUCTS:	
CC	-!- Event=Alternative splicing; Named isoforms=2;	
CC	-!- Name=R08934-1; Sequence=Displayed;	
CC	-!- Name=LMW;	
CC	-!- IsoID=P08934-2; Sequence=VSP_001265, VSP_001266;	
CC	-!- TISSUE SPECIFICITY: Plasma.	
CC	-!- PTM: Bradykinin is released from kininogen by plasma kallikrein.	
CC	-!- CLASSICAL: Rats express four types of kininogens: the classical HMW/LMW kininogens and two additional LMW-like kininogens: T-I and T-II.	
CC	-!- SIMILARITY: Contains 3 cystatin-like domains.	
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CC	DR EMBL; L29428; AAA41486.1; -.	
CC	DR EMBL; M11884; AAA41487.1; -.	
CC	DR EMBL; M14369; AAA41484.1; -.	
CC	DR EMBL; M1365; AAA41485.1; ALT_SEQ.	
CC	DR PIR; A25486; A22486.	
CC	DR PIR; A28055; A28055.	
CC	DR InterPro; IPR00010; Cystatin.	
CC	DR InterPro; IPR00329; Kininogen.	
CC	Pfam; PF00031; cystatin_3.	
CC	PRINTS; PR00334; KININOGEN.	
CC	SMART; SM00043; CY_3.	
CC	PROSITE; PS00287; Cystatin_2.	
CC	KW Glycoprotein; Plasma; Repat; Thiol protease inhibitor; Vasodilator; Bradykinin; Blood coagulation; Inflammatory response; Signal; Alternative splicing; Multigene family.	
FT	SIGNAL 1 18	
FT	CHAIN 19 639	KININOGEN.
FT	CHAIN 19 380	KININOGEN HEAVY CHAIN.
FT	PEPTIDE 381 389	KININOGEN LIGHT CHAIN.
FT	CHAIN 390 639	BRADYKININ.
FT	DOMAIN 19 136	CYSTATIN-LIKE 1.
FT	DOMAIN 137 258	CYSTATIN-LIKE 2.
FT	DOMAIN 259 380	CYSTATIN-LIKE 3.
FT	DOMAIN 439 514	HIS-RICH.
FT	DISULFID 28 609	INTERCHAIN (BY SIMILARITY).
FT	DISULFID 83 94	BY SIMILARITY.
FT	DISULFID 107 126	BY SIMILARITY.
FT	DISULFID 142 145	BY SIMILARITY.
FT	DISULFID 206 218	BY SIMILARITY.
FT	DISULFID 229 248	BY SIMILARITY.
FT	DISULFID 264 267	BY SIMILARITY.
FT	DISULFID 328 340	BY SIMILARITY.
FT	DISULFID 351 370	BY SIMILARITY.
FT	CARBONYD 82 82	N-LINKED (GLCNAC, .) (POTENTIAL).
FT	CARBONYD 127 127	N-LINKED (GLCNAC, .) (POTENTIAL).
FT	CARBONYD 169 169	N-LINKED (GLCNAC, .) (POTENTIAL).
FT	CARBONYD 205 205	N-LINKED (GLCNAC, .) (POTENTIAL).
FT	CARBONYD 294 294	N-LINKED (GLCNAC, .) (POTENTIAL).
FT	CARBONYD 529 529	N-LINKED (GLCNAC, .) (POTENTIAL).
FT	VARSPLIC 402 433	VPSYKARVQERDPNEQQPIHGWLHKQ > RLUNN CYKGRLKAGPAPERQEASTVTP (in isoform LMW).
FT	VARSPLIC 434 639	/FTId=VSP_001265. Missing (in isoform LMW).
FT	CONFFLICT 61 61	FTID=vsp_001266. E -> K (IN REF. 2).
FT	SEQUENCE 639 AA; 70933 MW;	D317DF94FF56AF5 CRC64;
Query Match	64.5%	Score 426; DB 1; Length 639;

DISULFID	83	94	BY SIMILARITY.	Xu Y., Weiss M., Ikeda M., Liggett D., Helms A., Caux C., Lebecque S., Hamm C., Menon S., McAllanahan T., Gorman D., Zurawski G.; "Leukocystatin, a new class II cystatin expressed selectively by hematopoietic cells."					
DISULFID	107	125	BY SIMILARITY.	RT					
DISULFID	141	144	BY SIMILARITY.	RT					
DISULFID	205	217	BY SIMILARITY.	RT					
DISULFID	228	247	BY SIMILARITY.	RL					
DISULFID	263	266	BY SIMILARITY.	J. Biol. Chem. 273:16400-16408(1998).					
DISULFID	327	339	BY SIMILARITY.	- - FUNCTION: Inhibits papain and cathepsin L but with affinities lower than other cystatins. May play a role in immune regulation through inhibition of a unique target in the hematopoietic system.					
DISULFID	350	369	BY SIMILARITY.	CC					
CARBONYD	82	82	N-LINKED (GLCNAC. .) (POTENTIAL).	CC					
CARBONYD	126	126	N-LINKED (GLCNAC. .) (POTENTIAL).	CC					
CARBONYD	168	168	N-LINKED (GLCNAC. .) (POTENTIAL).	CC					
CARBONYD	204	204	N-LINKED (GLCNAC. .) (POTENTIAL).	CC					
CARBONYD	326	326	N-LINKED (GLCNAC. .) (POTENTIAL).	CC					
CONFLICT	26	28	LNC -> MDR (IN REF. 2).	CC					
FT	CONFICT	55	V -> L (IN REF. 2).	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation in the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).					
FT	CONFICT	61	E -> K (IN REF. 1).	CC					
FT	CONFICT	83	C -> Y (IN REF. 3).	CC					
FT	CONFICT	166	S -> F (IN REF. 2 AND 3).	CC					
FT	CONFICT	179	REV -> TKI (IN REF. 2).	CC					
FT	CONFICT	193	N -> D (IN REF. 2).	CC					
FT	CONFICT	212	S -> F (IN REF. 2).	DR					
FT	CONFICT	214	R -> H (IN REF. 3).	DR					
FT	CONFICT	229	T -> R (IN REF. 2).	DR					
FT	CONFICT	233	H -> Y (IN REF. 2).	MGI:1248217; Cst7.					
FT	CONFICT	257	E -> S (IN REF. 2).	DR					
FT	CONFICT	262	N -> K (IN REF. 2).	DR					
FT	CONFICT	264	R -> F (IN REF. 2).	DR					
FT	CONFICT	268	RE -> KN (IN REF. 2).	DR					
FT	CONFICT	295	I -> L (IN REF. 2).	DR					
FT	CONFICT	314	VI -> TN (IN REF. 2).	DR					
FT	CONFICT	331	SK -> TN (IN REF. 2).	DR					
FT	CONFICT	389	R -> Q (IN REF. 2).	DR					
FT	CONFICT	414	R -> G (IN REF. 2 AND 3).	DR					
FT	CONFICT	415	A -> L (IN REF. 2).	DR					
FT	CONFICT	420	DH -> ER (IN REF. 3).	DR					
FT	CONFICT	430	P -> S (IN REF. 1).	DR					
SQ	SEQUENCE	430 AA;	FABBB78FAF4723C3 CRC64;	DR					
Query Match		60.8%	Score 401; DB 1; Length 430;	Query Match		26.5%	Score 175; DB 1; Length 144;		
Best Local Similarity		61.3%	Pred. No. 6.3e-31;	Best Local Similarity		34.4%	Pred. No. 6.8e-10;		
Matches		14	Mismatches 33; Indels 0; Gaps 0;	Matches		23; Mismatches 49; Indels 8; Gaps 4;			
Qy		1	GKDFVQPPTKICVGCPDPDIPTNSPELEETHTITKLNAENNATYFKIDNIVKKARVQVVA 60	Qy	2	KDFVQPPTKICVGCPDPDIPTNSPELEETHTITKLNAENNATYFKIDNIVKKARVQVVA 61			
Db		252	GDDLFELPLPQCRGCPREIPSLKEAGHSIAQLNQHNFYFYKDITVKKTSQV 311	Db	27	KDFVQPPTKICVGCPDPDIPTNSPELEETHTITKLNAENNATYFKIDNIVKKARVQVVA 83			
Qy		61	AGKRYFIDFVARETTCSKSENELTSETKXKGOSLDNCNAEVYYVPWEEKIYPTVNCP 120	Qy	62	GKXKYPIDEVARBTCSKSENELTSETKXKGOSLDNCNAEVYYVPWEEKIYPTVNCP 117			
Db		312	AGVYVTFIARETNGSKQSKTEFLADCFXHLGOSLNCRANTVMRPEWKVPTVRQA 371	Db	84	GLKYMLEVKGIRTTCSTXMHQD-DNCDFQTNPALKTLYCYSEWVTPWLHSPEPVVL 142			
Qy		121	LGM 123	Qy	118	CQ 119			
Db		372	LDM 374	Db	143	CQ 144			
RESULT 11					RESULT 11				
CYTF_MOUSE STANDARD;					CYTF_HUMAN STANDARD;				
ID		09UED4		09UED4	ID	09UED4		PRT	145 AA.
AC		076036		076036	AC	076036		PRTE	
DT	15-DEC-1998	(Rel. 37, Created)		15-DEC-1998 (Rel. 37, Created)	DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	15-DEC-1998	(Rel. 37, Last sequence update)		15-DEC-1998 (Rel. 37, Last sequence update)	DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DT	28-FEB-2003	(Rel. 41, Last annotation update)		Cystatin F precursor (Leukocystatin) (Cystatin 7) (Cystatin-like metastasis-associated protein) (CMAP).	DT	Cystatin F precursor (Leukocystatin) (Cystatin 7) (Cystatin-like metastasis-associated protein) (CMAP).			
DE					DE				
GN					GN				
CST7					CST7				
OS					OS				
Mammalia					Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OC				
OC					Mammalia; Butheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.				
OX					OX				
NCBI_TaxID	10080,				NCBI_TaxID	9606;			
RN	[1]				RN	SEQUENCE FROM N.A.			
RP					RP	Medline=9806133; PubMed=973383;			
RN					RN	Ni J., Fernandez M.A., Danielsson L., Chillakuru R.A., Zhang J., Grubb A., Su J., Gantz R., Abramson M.;			
RX					RX	"Cystatin F is a glycosylated human low molecular weight cysteine			
RA					RA	Halfon S., Ford J., Foster J., Dowling L., Lucian L., Sterling M.,			

[1] RN SEQUENCE FROM N.A.
 RP MEDLINE=97150844; PubMed=8995380;
 RX Sotiropoulou G., Anisowicz A., Sager R.;
 RA "Identification, cloning, and characterization of cystatin M, a novel
 RT cysteine proteinase inhibitor, down-regulated in breast cancer.";
 RL J. Biol. Chem. 272:903-910(1997).
 RN [2]
 SEQUENCE FROM N.A.
 RP TISSUE=Prostate;
 RX MEDLINE=22368257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Feingold E.A., Hernandez M.A., Grubbs A., Su J.,
 RA Yu G.L., Li Y., Parmelee D., Xing L., Coleman T.A., Gantz S.,
 RA Thotakura R., Nguyen N., Hesselberg M., Gentz R.;
 RA "Cystatin E is a novel human cysteine proteinase inhibitor with
 RT structural resemblance to family 2 cystatins";
 RL J. Biol. Chem. 272:10853-10858(1997).
 RN [3]
 SEQUENCE FROM N.A.
 RP
 RC TISSUE=Prostate;
 RX MEDLINE=97150844; PubMed=8995380;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,
 RA Altzman S.P., Zeerberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.P., Jordan R., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.J., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mulahay S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarate P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villaia M., Muzny D.M., Stoddergren B.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Rodriguez R.W., Toufic J.W., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schneirach A., Schein J.B., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP CHARACTERIZATION, AND TISSUE SPECIFICITY.
 RX MEDLINE=21246880; PubMed=1134857;
 RA Zeeuw P.L., Van Viljoen-Williams I.M., Jansen B.J., Sotiropoulou G.,
 RA Curfs J.H., Meis J.F., Janssen J.J., Van Ruissen F., Schalwijk J.,
 RT "Cystatin M/E expression is restricted to differentiated epidermal
 keratinocytes and sweat glands: a new skin-specific proteinase
 inhibitor that is a target for cross-linking by transglutaminase.";
 RL J. Invest. Dermatol. 116:693-701(2001).
 -I- FUNCTION: Shows moderate inhibition of cathepsin B but is not
 active against cathepsin C.
 -I- SUBCELLULAR LOCATION: Secreted.
 -I- TISSUE SPECIFICITY: Restricted to the stratum granulosum of normal
 skin, the stratum granulosum/spinosum of psoriatic skin, and the
 secretory coils of eccrine sweat glands. Low expression levels are
 found in the nasal cavity.
 CC -I- PIM: Substrate for transglutaminases. Acts as an acyl acceptor but
 CC not as an acyl donor.
 CC -I- SIMILARITY: Belongs to the cystatin family.

[2] RN SEQUENCE FROM N.A., SEQUENCE OF 66-83, AND CHARACTERIZATION.
 RP TISSUE=Cerebrospinal fluid, and Choroid plexus;
 RX MEDLINE=98091199; PubMed=934110;
 RA Olsson S.-L., Ek B., Wilm M., Broberg S., Rask L., Bjocsk I.;
 DB Cystatin C precursor (Colstrum thiol proteinase inhibitor).
 GN CST3.
 OS Bos taurus (Bovine).
 OC Bovidae; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC NCBI-TaxID=9913;
 RX OR

[1] RN SEQUENCE FROM N.A., SEQUENCE OF 66-83, AND CHARACTERIZATION.
 RP TISSUE=Cerebrospinal fluid, and Choroid plexus;
 RX MEDLINE=98091199; PubMed=934110;
 RA Olsson S.-L., Ek B., Wilm M., Broberg S., Rask L., Bjocsk I.;
 RT "Molecular cloning and N-terminal analysis of bovine cystatin C
 identification of a full-length N-terminal region.";
 RT Biochim. Biophys. Acta 1343:203-210(1997).
 RN PP SEQUENCE OF 37-148.
 RX MEDLINE=85231205; PubMed=3891407;

[2] RN PP SEQUENCE OF 37-148.
 RX MEDLINE=85231205; PubMed=3891407;
 RA Hirada M., Tsunashima S., Sakiyama F., Niinobe M., Fujii S.;
 RT "Complete amino acid sequence of bovine colosporin low-Mr cysteine
 proteinase inhibitor.";
 RT PEPS Lett. 186:41-45(1985).

[CC] CC -I- FUNCTION: This is a thiol proteinase inhibitor.
 CC -I- MASS SPECTROMETRY: MW=13420; METHOD=MALDI.
 CC -I- SIMILARITY: Belongs to the cystatin family.

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 or send an email to license@isb-sib.ch).
 CC DR EMBL; U62800; AAB06566; 1...
 DR EMBL; U81233; AAB1305; 1...
 DR EMBL; BC03134; AAH31334; 1...
 DR HSSP; P01038; 1CPW; 1...
 DR EMBL; Y10811; CAA1771; 1...
 DR HSSP; P01034; 1G96.

DR InterPro; IPR000010; Cystatin.
 DR Pfam; PF00031; cystatin; 1.
 DR SMART; SM00043; CY; 1.
 DR PROSITE; PS00287; CYSTATIN; 1.
 KW Thiol protease inhibitor; Signal; Pyroglutamyl carboxylic acid.
 FT SIGNAL 1 30 PROBABLE.
 CYSTATIN C.
 FT CHAIN 31 148 PYRROLIDONE CARBOXYLIC ACID (PROBABLE).
 MOD RES 31 31 REACTIVE SITE.
 ACT SITE 40 40 SECONDARY AREA OF CONTACT.
 SITE 84 88 BY SIMILARITY.
 DISULFID 102 112 BY SIMILARITY.
 DISULFID 126 146 BY SIMILARITY.
 SEQUENCE 148 AA; 16265 MW; BE740FE37CFB9F0E CRC64;
 DR DISULFID 123 143 BY SIMILARITY.
 SQ SEQUENCE 146 AA; 15857 MW; F03BB774A29DF26 CRC64;

Query Match 20.2%; Score 133.5; DB 1; Length 146;
 Best Local Similarity 29.0%; Prod. No. 6.3e-06;
 Matches 31; Conservative 21; Mismatches 48; Indels 7; Gaps 3;

Qy 6 QPPTKICVCPRTDIPNTSPELEETLTHITKLNAENNATYFKIDNTVKARVQVAGKKY 65
 Db 31 KPPR-LVGGPMDSAEEGVRALDFAVSEYNKASNDMYHSLAQVTRAKQIVAGVNY 88

Qy 66 FIDPVARETTCSKESNEELTESC--ETTKLGOSLDNCNAEVYYVWPE 109
 Db 89 FLDVBLGRITCTK-TOPNLNDNPHEQPHLKRAFCSFQIYTVPWQ 133

Query Match 20.6%; Score 136; DB 1; Length 148;
 Best Local Similarity 30.6%; Prod. No. 3.7e-16;
 Matches 34; Conservative 22; Mismatches 31; Indels 24; Gaps 5;

RESULT 15
 CYTC_MACMU STANDARD; PRT; 146 AA.

Qy 22 NSPELBETLTHITKLNAENNATYFKIDNTVKARVQVAGKKYFIDPVARETTCSKESN 81
 Db 48 NEEGVQALSAFSVSEPFKRSNDAYQSRVVRVTRASKQVSGMNYFIDVLEGRITCTK-S 105
 FT 15-JUL-1998 (Rel. 36, Created)
 FT 15-JUL-1998 (Rel. 36, Last sequence update)
 FT 28-FEB-2003 (Rel. 41, Last annotation update)

Qy 82 EEDTESC-----ETKRLGSQSLDCNAEYVVWPWKKIYPTVN----CQ 119
 Db 106 QANLDSCPFPNQPHLKREKL---CSFQVYVUPHNN---TINLVKFCQ 147

OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Macaca.
 NCBI TaxID:9544; XN_01052; AAH64051.1; -.

RN [1] SEQUENCE FROM N.A.
 RP MEDLINE=97054523; PubMed=8898820;
 RXN WEI L.H.; Walker L.C.; Levy E.;
 RA "Cystatin C. Icelandic-like mutation in an animal model of cerebrovascular beta-amyloidosis.";
 RT Stroke 27:2080-2085 (1996).
 CC !- FUNCTION: As an inhibitor of cysteine Proteinases, this protein is thought to serve an important physiological role as a local regulator of this enzyme activity.
 CC !- SIMILARITY: Belongs to the cystatin family.

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RN [1] SEQUENCE FROM N.A.
 RP MEDLINE=97054523; PubMed=8898820;
 RXN WEI L.H.; Walker L.C.; Levy E.;
 RA "Cystatin C. Icelandic-like mutation in an animal model of cerebrovascular beta-amyloidosis.";
 RT Stroke 27:2080-2085 (1996).
 CC !- FUNCTION: As an inhibitor of cysteine proteinases, this protein is thought to serve an important physiological role as a local regulator of this enzyme activity.
 CC !- SIMILARITY: Belongs to the cystatin family.

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CC PROSITE; PS00287; CYSTATIN; 1.
 DR HSSP; PF00031; cystatin; 1.
 DR SMART; SM00043; CY; 1.
 DR InterPro; IPR00010; Cystatin.
 DR PFam; PF00031; cystatin; 1.

DR DISULFID 123 143 BY SIMILARITY.
 SQ SEQUENCE 146 AA; 15946 MW; 08196353C0306AA3 CRC64;

Query Match 20.1%; Score 132.5; DB 1; Length 146;
 Best Local Similarity 29.0%; Prod. No. 7.8e-06;
 Matches 29; Conservative 21; Mismatches 45; Indels 5; Gaps 2;

Qy 13 VGCPRDIPNTSPELEETLTHITKLNAENNATYFKIDNTVKARVQVAGKKYFIDVVAR 72
 Db 36 LGGPMDSAEEGVRALDFAVSEYNKASNDMYHSLAQVTRAKQIVAGVNYFLDVMG 95

FT 73 ETTCVKESNEELTESC--ETKLGOSLDNCNAEVYYVWPE 109

Db 96 RTTCTK--NQPNLDNCPPHEQPHLKEKAFCSFQIXSVPMQ 133

Search completed: September 24, 2004, 14:09:12
Job time : 23.364 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 24, 2004, 14:05:18 ; Search time 35.424 Seconds

(without alignments)
 1095.549 Million cell updates/sec

Title: US-10-661-784-1

Perfect score: 660

Sequence: 1 GRDFVQPPTKIVGCPRDIP.....YVVPWEKKIYPTVNQPLGM 123

Scoring table: BLOSUM62

GapOp 10.0 , GapExt 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

SPREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_micr:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriop:*

17: sp_archeap:*

Q98sr4 acipenser s

Q98sr3 acipenser s

Q9TY2 caenorhabdi

Q80126 cyprinus ca

Q9TY5 onchocerca

Q9jm84 mus musculu

Q8vnc1 rattus norv

Q16159 brugia malai

Q9u9al onchocerca

P06985 brugia malai

Q8sa95 sandersonia

Q8t0cy2 sarcophaga

Q25620 onchocerca

Q41825 zea mays (m

Q61973 caenorhabdi

Q44396 haemochirus

Q8rxu6 homo sapien

Q1108 acanthocheilus

Q8k5a3 rattus norvegicus

Q9fxn6 rabidopsis

Q8rxs7 arabidopsis

Q41906 arabidopsis

Q22202 arabidopsis

P93627 zea mays (m

Q41897 zea mays (m

Q9dap1 mus musculu

Q866wo nippotstrongylus

Q39270 brassica campestris

ALIGNMENTS

RESULT 1

Q7YRP6 PRELIMINARY; ID: Q7YRP6 PRELIMINARY;

AC: Q7YRP6; CREATED; DT: 01-OCT-2003 (TREMBLref), 25, Last sequence update)

DT: 01-OCT-2003 (TREMBLref), 25, Last annotation update)

DE: Low molecular weight kininogen (Fragment).

GN: Sus scrofa (Pig).

OS: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OC: NCBI_TaxID=9823;

RN: [1]

RP: SEQUENCE FROM N.A.

RA: Vonahme K.A., Fernando S.C., Ross J.A., Ashworth M.D., DeSilva U.,

RA: Malayer J.R., Geisert R.D.,

RT: "Porcine Endometrial and Conceptus Expression of Kininogens and Plasma

Kallikrein in Cyclic and Pregnant Gilts."

RL: Submitted (JUN-2003) to the EMBL/Genbank/DDBJ databases.

DR: EMBL:AY321363; AAP85260.1; -.

FT: NON_TER 140 AA; AAP85260.1; -.

FT: NON_TER 140 AA; 15650 MW; 177837836603F777 CRC64;

FT: NON_TER 140 AA; 140 MW; 177837836603F777 CRC64;

Query Match 61.2%; Score 404; DB 6; Length 140;
 Best Local Similarity 78.2%; Pred. No. 5, 4e-33;
 Matches 79; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

Query Match 22 NSPBLEEPLTHHTIKLNAAANNATFYKIDVYKARYVQVAGKRYFDVARETTCSXESN 81
 Best Local Similarity 78.2%; Pred. No. 5, 4e-33;
 Matches 79; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

Qy: 72 ELTESETKLUQGOSLDCAENATFYKIDVYKARYVQVAGKRYFDVARETTCSXESN 81
 Db: 1 DSSPLEEPLNHSIAKLNAAANNATFYKIGPVKETAVQVAGKYSIVFTARETTCSXESN 60

Qy: 82 ELTESETKLUQGOSLDCAENATFYKIDVYKARYVQVAGKRYFDVARETTCSXESN 122
 Db: 61 ELTESETKLUQGOSLDCAENATFYKIDVYKARYVQVAGKRYFDVARETTCSXESN 101

RESULT 2

Description

Q7YRP6 sus scrofa

P70517 rattus norvegicus

Q6581 rattus norvegicus

Q7z4j8 homo sapiens

Q7zy91 xenopus laevis

Q7syh2 xenopus laevis

Q801e5 xenopus laevis

Q8epx9 mus musculus

Q8088 brachydanio

Q812z5 cyprinus carpio

Q8cb17 litomoeidae

Q8by72 mus musculus

Q8k397 mus musculus

Q9d1b1 mus musculus

SUMMARIES

* Query

No. Score

Match

Length

DB

ID

Score

Length

DB

ID

P70517	PRELIMINARY;	PRT;	423 AA.	
AC	P70517; 02, Created)			
DT	01-FEB-1997 (TREMBLrel. 02, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DR	Major acute phase alpha-1 protein precursor (Fragment).			
DE	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN				
RP	SEQUENCE FROM N.A.			
RA	Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.			
RN				
RP	SEQUENCE FROM N.A.			
RX	PubMed=85149311; Pubmed=2579644;			
RA	Cole T., Inglis A.S., Roxburgh C.M., Howlett G.J., Schreiber G.; "Major acute phase alpha-1 protein of the rat: structure, molecular cloning, and regulation of mRNA levels"; Biochem. Biophys. Res. Commun. 126:719-724 (1985).			
RX	PubMed=85127561; Pubmed=2578992;			
RA	Cole T., Inglis A.S., Roxburgh C.M., Howlett G.J., Schreiber G.; "Major acute phase alpha-1 protein of the rat is homologous to bovine kininogen and contains the sequence for bradykinin: its synthesis is regulated at the mRNA level.."; FEBS Lett. 182:57-61 (1985).			
RT	"Major acute-phase, alpha(1)-protein in the rat: structure, molecular cloning, and regulation of mRNA levels";			
RT	InterPro: IPR000010; Cystatin.			
RT	SMART: SM00043; CY_3.			
RN				
RP	SEQUENCE FROM N.A.			
RX	PubMed=85127561; Pubmed=2578992;			
RA	Cole T., Inglis A.S., Roxburgh C.M., Howlett G.J., Schreiber G.; "Major acute phase alpha-1 protein of the rat is homologous to bovine kininogen and contains the sequence for bradykinin: its synthesis is regulated at the mRNA level.."; FEBS Lett. 182:57-61 (1985).			
RT	"Major acute-phase, alpha(1)-protein in the rat: structure, molecular cloning, and regulation of mRNA levels";			
RT	InterPro: IPR000010; Cystatin.			
RT	SMART: SM00043; CY_3.			
RP	SEQUENCE FROM N.A.			
RX	PubMed=85127561; Pubmed=2578992;			
RA	Cole T., Inglis A.S., Roxburgh C.M., Howlett G.J., Schreiber G.; "Major acute phase alpha-1 protein of the rat is homologous to bovine kininogen and contains the sequence for bradykinin: its synthesis is regulated at the mRNA level.."; FEBS Lett. 182:57-61 (1985).			
RT	"Major acute-phase, alpha(1)-protein in the rat: structure, molecular cloning, and regulation of mRNA levels";			
RT	InterPro: IPR000010; Cystatin.			
RT	SMART: SM00043; CY_3.			
RP	SEQUENCE FROM N.A.			
RX	PubMed=85127561; Pubmed=2578992;			
RA	Cole T., Inglis A.S., Roxburgh C.M., Howlett G.J., Schreiber G.; "Major acute phase alpha-1 protein of the rat is homologous to bovine kininogen and contains the sequence for bradykinin: its synthesis is regulated at the mRNA level.."; FEBS Lett. 182:57-61 (1985).			
RT	"Major acute-phase, alpha(1)-protein in the rat: structure, molecular cloning, and regulation of mRNA levels";			
RT	InterPro: IPR000010; Cystatin.			
RT	SMART: SM00043; CY_3.			
KW	NON_TER	1	1	POTENTIAL.
FT	SIGNAL	<1	11	POTENTIAL.
FT	CHAIN	12	423	POTENTIAL.
FT	CHAIN	371	379	POTENTIAL.
SQ	SEQUENCE 423 AA; 46905 MW; F9E8ED3138547949 CRC64;			
Query Match	Score 402; DB 11; Length 423;			
Best Local Similarity	60.9%; Pred. No. 3.1e-32;			
Matches	76; Conservative 14; Mismatches 33; Indels 0; Gaps 0;			
QY	1. GKDVFQPTKIVGCPDPIDPNSPELETLITKLNAENNATFYKIDNVKKARVQV 60			RESULT 4
Db	GDDLFELLPKRNCRGCPEIPDVSPKELAHLGSIARLNQHNFYFKIDVVKATSQVY 304			
QY	61. AGKRYFIDFVARETTCSKESNBELTECETKLKGOSLDCNAEVTTYPWFKIYPTYNCP 120			
Db	312. AGVIVYVBFIARETNCQSKTELTADECYKLQGSINCNANVNTYRPWENKVYPTRCQA 371			
QY	121. LGM 123			
Db	372. LDM 374			
RP	SEQUENCE FROM N.A.			
RX	STRAIN=C57BL/6J; TISSUE=Embryo; MEDLINE=2105660; Published=1217851;			
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hirai A., Fukunishi Y., Konno H., Andachi J., Fukuda S., Aizawa M., Izawa M., Nishi K., Kiyosawa H., Yamamoto I., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cassava T., Saito R., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kueh P., Lewis S., Matsuo Y., Nikaido I., Peelo G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,			
RP	SEQUENCE FROM N.A.			
RX	Morita M., Arakawa H., Yoshiuchi N.			
RA	"A novel cystatin-associated gene."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
RL	RN			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
RL	RN			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
RL	RN			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
RL	RN			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
RL	RN			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
RL	RN			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
RL	RN			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
RL	RN			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
RL	RN			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
RL	RN			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
RL	RN			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
RL	RN			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
RL	RN			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
RL	RN			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
RL	RN			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
RL	RN			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
RL	RN			
RN	[2]			
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RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
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RT	Mon Sep 27 08:32:56 2004			
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RT	Mon Sep 27 08:32:56 2004			
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RT	Mon Sep 27 08:32:56 2004			
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RN	[2]			
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RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
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RN	[2]			
RP	SEQUENCE FROM N.A.			
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RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
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RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
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RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
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RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
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RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
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RT	Mon Sep 27 08:32:56 2004			
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RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
RL	RN			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
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RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
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RT	Mon Sep 27 08:32:56 2004			
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RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
RL	RN			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
RL	RN			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
RL	RN			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
RL	RN			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
RL	RN			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
RL	RN			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
RL	RN			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	RN			
RA	Mon Sep 27 08:32:56 2004			
RT	Mon Sep 27 08:32:56 2004			
RL				

RESULT 5
Q7Z4J8 PRELIMINARY; PRT; 167 AA.
ID Q7Z4J8
AC Q7Z4J8;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
RA Kalline N.; Chen X.; Rolfs A.; Halleck A.; Eisenstein S.;
RA Koundinya M.; Raphael J.; Moreira D.; Kelley T.; LaBeer J.; Lin Y.;
RA Phelan M.; Farmer A.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT009825; AAP888227; -;
SEQUENCE 167 AA; 18857 MW; E33902545BD60177 CRC64;

Query Match 25.1%; Score 165 5; DB 4; Length 167;
Best Local Similarity 32.5%; Pred. No. 7.5e-09;
Matches 37; Conservative 22; Mismatches 50; Indels 5; Gaps 3;

Qy 9 TKICVCPRDIPNTSPEELTHITKUNAENNATFYKIDNVKKARVOVAGKXPFID 68
Db 54 SRVKSGFPKTKITNDPGVLQAARYSEKFUNCTNDMFLPKESRTRALQVGLKMLE 113

Qy 69 FVARETTCSKSNEELTESCB---TKKLGSOSLDNAEYVVPWERKI - VPTYNC 118
Db 114 VEIGRTICKNQHLRL-DCCDFQTNTLQLTSCYSEWVNPWLQHFVFPVLRC 166

RESULT 6
Q7ZY91 PRELIMINARY; PRT; 462 AA.
ID Q7ZY91
AC Q7ZY91;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 23, Last annotation update)
DB Similar to fetuin B.
OS Xenopus laevis (African clawed frog).
OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TAXID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Embryo;
RA Klein S.; Straubberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR BC043891; AAH43891.1; -;
DR GO; GO:0004869; P:cytine protease inhibitor activity; IEA.
DR InterPro; IPR000010; Cystatin.
DR PFAM; PF00031; cystatin; 2.
DR SMART; SM00043; Cy; 2.
SQ SEQUENCE 462 AA; 53185 MW; D7BAD339961739FB CRC64;

Query Match 23.1%; Score 152.5; DB 13; Length 462;
Best Local Similarity 38.8%; Pred. No. 5e-07;
Matches 33; Conservative 13; Mismatches 34; Indels 5; Gaps 2;

Qy 8 PTKICVCPRDIPNTSPEELTHITKUNAENNATFYKIDNVKKARVOVAGK 63
Db 142 PGVILSICP-DCPTANEETITPITEADTLIAEYNKDSNNTRYFKIDDHIERVRSQTVVGP 200

Qy 64 KYFIDFVARETTCSKSNEELTESC 88
Db 201 SYFIQFTIKETDCMKTOENVULSNC 225

RESULT 7
Q7SYH2 PRELIMINARY; PRT; 462 AA.
ID Q7SYH2
AC Q7SYH2;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Cystatin domain fetuin-like protein.
OS Xenopus laevis (African clawed frog).
OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TAXID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Ventral midgut;
RA Costa R.M.B.; Mason J.; Lee M.; Amaya E.; Zorn A.M.;
RA "Novel gene expression domains reveal early patterning of the Xenopus endoderm.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR AY260132; AAP8289.1; -;
SQ SEQUENCE 462 AA; 53186 MW; 796f92774CC27721 CRC64;

Query Match 23.1%; Score 152.5; DB 13; Length 462;
Best Local Similarity 38.8%; Pred. No. 5e-07;
Matches 33; Conservative 13; Mismatches 34; Indels 5; Gaps 2;

Qy 8 PTKICVCPRDIPNTSPEELTHITKUNAENNATFYKIDNVKKARVOVAGK 63
Db 142 PGVILSICP-DCPTANEETITPITEADTLIAEYNKDSNNTRYFKIDDHIERVRSQTVVGP 200

Qy 64 KYFIDFVARETTCSKSNEELTESC 88
Db 201 SYFIQFTIKETDCMKTOENVULSNC 225

RESULT 8		FT VARIANT 16 16 A ~> G.
Q801E5	ID PRELIMINARY;	FT; 465 AA.
AC Q801E5;		
DT 01-JUN-2003 (TREMBLrel. 24, Created)		
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)		
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE Hypothetical histidine-rich protein (Fragment).		
OS Xenopus laevis (African clawed frog).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;		
OC Xenopodaee; Xenopus.		
OX NCBI_TaxID=8355;		
RN [1]		
RP SEQUENCE FROM N.A.; PubMed=12591597;		
RX MEDLINE=22480013; PubMed=12591597;		
RX Chen Y., Jurgens K., Hollemann T., Claussen M., Ramadori G.,		
RA Pieler T.;		
RT "Cell-autonomous and signal-dependent expression of liver and embryo.", Mech. Dev. 120:277-288 (2003).		
RT Embryo.;		
RL DR IPR00031; Cystatin.		
DR GO:0004869; P:cytostine protease inhibitor activity; IEA.		
DR InterPro; IPR00001; Cystatin.		
DR SMART; SM00043; CY; 2.		
KW Hypothetical protein.		
FT NON_TER 1 1		
SQ SEQUENCE 465 AA; 53528 MW; 0B403AB4F78BBFD4 CRC64;		
Query Match Score 23.1%; Score 152.5%; DB 13; Length 465;		
Best Local Similarity 38.8%; Pred. No. 5e-07;		
Matches 33; Conservative 13; Mismatches 34; Indels 5; Gaps 2;		
Qy 8 PTKICVCPDIFTPTNSPELEETLTHTH----TTKLNAAENNATFYFKIDNYTKARYQVVAASK 63		
Db 145 PEGVILSTOP-DGPTANBPIPTPTEATLTAEYNRDSNNTRYFKIDHIERVRSQWVVGPF 203		
Qy 64 KYFIDPVARETTCOKSKESENELTESC 88		
Db 204 SYFOFTIKETDCMKTQENVVLSNC 228		
RESULT 9		
Q9EPX9	ID PRELIMINARY;	FT; 140 AA.
AC Q9EPX9;		
DT 01-MAR-2001 (TREMBLrel. 16, Created)		
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)		
DE Cystatin_C.		
OS Mus musculus (Mouse).		
OC Mammalia; Eutheria; Chordata; Rodentia; Sciurognathii; Muridae; Mus.		
OX NCBI_TaxID=10090;		
RN [1]		
RP SEQUENCE FROM N.A.		
RC STRAIN-BALB/C;		
RX MEDLINE=211010502; PubMed=11144350;		
RA Taupin P.J., Ray J., Fischer W.H., Suhr S.T., Hakansson K., Grubb A., Gage F.H.;		
RA RT "RGP-2: Responsive neural stem cell proliferation requires Ctgf, a novel autoocrine/paracrine cofactor.";		
RL Neuron 28:385-397(2000).		
DR EMBL; AP311741; AAQ40283.1.-.		
DR HSSP; P01034; 1096.		
DR GO:0004869; P:cytostine Protease inhibitor activity; IEA.		
DR InterPro; IPR000010; Cystatin.		
DR SMART; SM00043; CY; 1.		
DR PROSITE; PS00287; CYSTATIN_1.		
FT CHAIN 21		

Db	154	CPDCPSPIDLSNPSALEARTESLAFENSKSPSKRY-ELVKVTKANQWSPGPAYVEYL	I	212
[1]	SEQUENCE FROM N.A.			
TSAI P.-L., Chang G.-D., Huang C.-J.; "Purification and cloning of carp fetuin"; Submitted (JAN-2001) to the EMBL/Germany/DBDU databases.	EMBL; AY225965; AA074862.1;			
GO; GO:0005814; C:microtubule; IFA.	GO; GO:004869; P:cytoseine Protease inhibitor activity; IFA.			
SMART; SM00043; CY; PROSITE; PS00028; TUBULIN_B_AUTOREG; 1.0	GO; GO:0007018; P:structural molecule activity; IFA.			
SEQUENCE 464 AA; 51698 MW;	7A54F71E44050895 CRC64;			
Query Match 17.9%; Score 118; DB 13; Length 464;	Best Local Similarity 24.2%; Pred. No. 0.0015;	Gaps 5;		
Matches 31; Conservative 27; Mismatches 50; Indels 20; Gaps 5;				
2Y 12 CVGPRDFNTNSPLEETLTHITKLNAENNATYPKIDDNVKARVQ-WVAGKXYPIDEV 70				
Db 142 CPDCPGILFLHDPKGLESTKTAQLQFNKESDHSKYFKLMEVGRISTONWFGSQFFSQA 201				
QY 71 ARETTCSKE--SNEBELTS-----CETKRKG-QSLDCNAEVTVV----PWEK 111				
Db 202 IMETINCNKEAPQNNEESCKALCGEKAryGFCKSTKVGLIEPEPECEIYPAKINTHPWP 261				
2Y 112 IYPTIVNQ 119				
Db 262 AQSRRDCK 269				
Query Match 17.2%; Score 113 5; DB 5; Length 148;	Best Local Similarity 34.1%; Pred. No. 0.0011;	Gaps 3;		
Matches 30; Conservative 16; Mismatches 37; Indels 5; Gaps 3;				
Q8CB17 PRELIMINARY; PRT; 388 AA.				
AC QBBB17; PRELIMINARY; PRT; 388 AA.				
1-MAR-2003 (TREMBrel. 23, Created)				
01-MAR-2003 (TREMBrel. 23, Last sequence update)				
01-OCT-2003 (TREMBrel. 25, Last annotation update)				
Fetuin beta.				
DE				
Mus musculus (Mouse).				
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NCBI_TaxID=10090; OX				
RESULT 12				
Q8CB17 PRELIMINARY; PRT; 388 AA.				
AC QBBB17; PRELIMINARY; PRT; 388 AA.				
01-MAR-2003 (TREMBrel. 23, Created)				
01-MAR-2003 (TREMBrel. 23, Last sequence update)				
01-OCT-2003 (TREMBrel. 25, Last annotation update)				
Fetuin beta.				
DE				
Nature 420:563-573 (2002).				
EMBL; A037043; BAC19682.1; -.				
Mus musculus (Mouse).				
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NCBI_TaxID=10090; OX				
RN				
SEQUENCE FROM N.A.				
STRAIN=57BL/6J; TISSUE=Vagina;				
MEDLINE=22354683; PubMed=12466851;				
The FANTOM Consortium,				
the RIKEN Genome Exploration Research Group Phase I & II Team;				
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."				
Nature 420:563-573 (2002).				
EMBL; A037043; BAC19682.1; -.				
SEQUENCE 388 AA; 42742 MW;	78CPAD73A8D8D22 CRC64;			
InterPro; IPRO00010; Cystatin.				
InterPro; IPRO01363; Fetuin.				
PFan; PF00031; cystatin; 2.				
SMART; SM00043; CY; PROSITE; PS010254; FETUIN 1; 1.				
PROSITE; PS01025; FETUIN 2; 1.				
SEQUENCE 388 AA; 42742 MW;	78CPAD73A8D8D22 CRC64;			
Query Match 17.5%; Score 115 5; DB 11; Length 388;				
Best Local Similarity 26.7%; Pred. No. 0.0022;				
Matches 31; Conservative 24; Mismatches 48; Indels 13; Gaps 4;				
Q8CB17 PRELIMINARY; PRT; 388 AA.				
AC QBBB17; PRELIMINARY; PRT; 388 AA.				
01-JUN-2003 (TREMBrel. 24, Created)				
01-JUN-2003 (TREMBrel. 24, Last sequence update)				
Fetuin beta.				
DE				
Cystatin-like 1.				
OS Mus musculus (Mouse).				
OC				
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NCBI_TaxID=10090; OX				
RN				
SEQUENCE FROM N.A.				
TISSUE=Tessicell;				
RC				
MEDLINE=22388237; PubMed=12477932;				
RX				
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collinge F.S., Wagner L., Casavant T.L., Scheetz T.B., Altenschul S.F., Zeeberg B., Bustow K.H., Schaeffer C.F., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Bonaldo M.F., Casavant T.L., Scheetz T.B., Stapleton M., Soares M.B., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Lopez-N.A., Peters G.J., Abramson R.D., Mullaly S.J., Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H., Bosak S.A., McElwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
Q8CB17 PRELIMINARY; PRT; 388 AA.				
AC QBBB17; PRELIMINARY; PRT; 388 AA.				
01-OCT-2003 (TREMBrel. 25, Last annotation update)				
Fetuin beta.				
DE				
Cystatin-like 1.				
OS Mus musculus (Mouse).				
OC				
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NCBI_TaxID=10090; OX				
RN				
SEQUENCE FROM N.A.				
TISSUE=Tessicell;				
RC				
MEDLINE=22388237; PubMed=12477932;				
RX				
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collinge F.S., Wagner L., Casavant T.L., Scheetz T.B., Altenschul S.F., Zeeberg B., Bustow K.H., Schaeffer C.F., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Bonaldo M.F., Casavant T.L., Scheetz T.B., Stapleton M., Soares M.B., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Lopez-N.A., Peters G.J., Abramson R.D., Mullaly S.J., Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
Q8CB17 PRELIMINARY; PRT; 388 AA.				
AC QBBB17; PRELIMINARY; PRT; 388 AA.				
01-OCT-2003 (TREMBrel. 25, Last annotation update)				
Fetuin beta.				
DE				
Cystatin-like 1.				
OS Mus musculus (Mouse).				
OC				
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NCBI_TaxID=10090; OX				
RN				
SEQUENCE FROM N.A.				
TISSUE=Tessicell;				
RC				
MEDLINE=22388237; PubMed=12477932;				
RX				
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collinge F.S., Wagner L., Casavant T.L., Scheetz T.B., Altenschul S.F., Zeeberg B., Bustow K.H., Schaeffer C.F., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Bonaldo M.F., Casavant T.L., Scheetz T.B., Stapleton M., Soares M.B., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Lopez-N.A., Peters G.J., Abramson R.D., Mullaly S.J., Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
Q8CB17 PRELIMINARY; PRT; 388 AA.				
AC QBBB17; PRELIMINARY; PRT; 388 AA.				
01-OCT-2003 (TREMBrel. 25, Last annotation update)				
Fetuin beta.				
DE				
Cystatin-like 1.				
OS Mus musculus (Mouse).				
OC				
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NCBI_TaxID=10090; OX				
RN				
SEQUENCE FROM N.A.				
TISSUE=Tessicell;				
RC				
MEDLINE=22388237; PubMed=12477932;				
RX				
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collinge F.S., Wagner L., Casavant T.L., Scheetz T.B., Altenschul S.F., Zeeberg B., Bustow K.H., Schaeffer C.F., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Bonaldo M.F., Casavant T.L., Scheetz T.B., Stapleton M., Soares M.B., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Lopez-N.A., Peters G.J., Abramson R.D., Mullaly S.J., Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
Q8CB17 PRELIMINARY; PRT; 388 AA.				
AC QBBB17; PRELIMINARY; PRT; 388 AA.				
01-OCT-2003 (TREMBrel. 25, Last annotation update)				
Fetuin beta.				
DE				
Cystatin-like 1.				
OS Mus musculus (Mouse).				
OC				
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NCBI_TaxID=10090; OX				
RN				
SEQUENCE FROM N.A.				
TISSUE=Tessicell;				
RC				
MEDLINE=22388237; PubMed=12477932;				
RX				
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collinge F.S., Wagner L., Casavant T.L., Scheetz T.B., Altenschul S.F., Zeeberg B., Bustow K.H., Schaeffer C.F., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Bonaldo M.F., Casavant T.L., Scheetz T.B., Stapleton M., Soares M.B., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Lopez-N.A., Peters G.J., Abramson R.D., Mullaly S.J., Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
Q8CB17 PRELIMINARY; PRT; 388 AA.				
AC QBBB17; PRELIMINARY; PRT; 388 AA.				
01-OCT-2003 (TREMBrel. 25, Last annotation update)				
Fetuin beta.				
DE				
Cystatin-like 1.				
OS Mus musculus (Mouse).				
OC				
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NCBI_TaxID=10090; OX				
RN				
SEQUENCE FROM N.A.				
TISSUE=Tessicell;				
RC				
MEDLINE=22388237; PubMed=12477932;				
RX				
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collinge F.S., Wagner L., Casavant T.L., Scheetz T.B., Altenschul S.F., Zeeberg B., Bustow K.H., Schaeffer C.F., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Bonaldo M.F., Casavant T.L., Scheetz T.B., Stapleton M., Soares M.B., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Lopez-N.A., Peters G.J., Abramson R.D., Mullaly S.J., Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
Q8CB17 PRELIMINARY; PRT; 388 AA.				
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Q8CB17 PRELIMINARY; PRT; 388 AA.				
AC QBBB17; PRELIMINARY; PRT; 388 AA.				
01-OCT-2003 (TREMBrel. 25, Last annotation update)				
Fetuin beta.				
DE				
Cystatin-like 1.				
OS Mus musculus (Mouse).				
OC				
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NCBI_TaxID=10090; OX				
RN				
SEQUENCE FROM N.A.				
TISSUE=Tessicell;				
RC				
MEDLINE=22388237; PubMed=12477932;				
RX				
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collinge F.S., Wagner L., Casavant T.L., Scheetz T.B., Altenschul S.F., Zeeberg B., Bustow K.H., Schaeffer C.F., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Bonaldo M.F., Casavant T.L., Scheetz T.B., Stapleton M., Soares M.B., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Lopez-N.A., Peters G.J., Abramson R.D., Mullaly S.J., Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
Q8CB17 PRELIMINARY; PRT; 388 AA.				
AC QBBB17; PRELIMINARY; PRT; 388 AA.				
01-OCT-2003 (TREMBrel. 25, Last annotation update)				
Fetuin beta.				
DE				
Cystatin-like 1.				
OS Mus musculus (Mouse).				
OC				
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NCBI_TaxID=10090; OX				
RN				
SEQUENCE FROM N.A.				
TISSUE=Tessicell;				
RC				
MEDLINE=22388237; PubMed=12477932;				
RX				
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collinge F.S., Wagner L., Casavant T.L., Scheetz T.B., Altenschul S.F., Zeeberg B., Bustow K.H., Schaeffer C.F., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Bonaldo M.F., Casavant T.L., Scheetz T.B., Stapleton M., Soares M.B., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Lopez-N.A., Peters G.J., Abramson R.D., Mullaly S.J., Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
Q8CB17 PRELIMINARY; PRT; 388 AA.				
AC QBBB17; PRELIMINARY; PRT; 388 AA.				
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NCBI_TaxID=10090; OX				
RN				
SEQUENCE FROM N.A.				
TISSUE=Tessicell;				
RC				
MEDLINE=22388237; PubMed=12477932;				
RX				
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AC QBBB17; PRELIMINARY; PRT; 388 AA.				
01-OCT-2003 (TREMBrel. 25, Last annotation update)				
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Cystatin-like 1.				
OS Mus musculus (Mouse).				
OC				
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NCBI_TaxID=10090; OX				
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SEQUENCE FROM N.A.				
TISSUE=Tessicell;				
RC				
MEDLINE=22388237; PubMed=12477932;				
RX				
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collinge F.S., Wagner L., Casavant T.L., Scheetz T.B., Altenschul S.F., Zeeberg B., Bustow K.H., Schaeffer C.F., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Bonaldo M.F., Casavant T.L., Scheetz T.B., Stapleton M., Soares M.B., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Lopez-N.A., Peters G.J., Abramson R.D., Mullaly S.J., Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
Q8CB17 PRELIMINARY; PRT; 388 AA.				
AC QBBB17; PRELIMINARY; PRT; 388 AA.				
01-OCT-2003 (TREMBrel. 25, Last annotation update)				
Fetuin beta.				
DE				
Cystatin-like 1.				
OS Mus musculus (Mouse).				
OC				

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton B., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Rodriguez M., Madan A.C., Young J.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimeswood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schneich A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.",
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testicle;
 RA Strausberg R.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC048641; AAH48646.1;
 GO; GO:0004869; P:cytosteine protease inhibitor activity; IEA.
 DR InterPro; IPR000010; Cystatin.
 DR InterPro; IPR003243; Cystatin_C/M.
 DR Pfam; PF00031; cystatin; 1.
 DR ProDom; PD001231; Cytstatin_C/M; 1.
 DR SMART; SM00043; CY; 1.
 SQ SEQUENCE 140 AA; 16199 MW; 32633E99C4697DA0 CRC64;
 Query Match Score 17.1%; Score 113; DB 11; Length 140;
 Best Local Similarity 29.4%; Pred. No. 0.0012;
 Matches 25; Conservative 18; Mismatches 38; Indels 4; Gaps 2;
 DR 4.4 INSTLHFFIRSTNNASNDTYYQVOKLIGOMQLTGVEYLTVKIGRCKKK-NETPK 101

Qy 26 LEETLHTITKINAENNATYFKIDNWKARRVQVYAGKRYFIDFYARETTCSKESNEELIT 85
 Db 4.4 ASCPLQSSKLRSLICKSLIKSVWP 126

Qy 86 ESC-ETTKLGOSLDNAEVVVPW 108
 Db 102 ASCPLQSSKLRSLICKSLIKSVWP 126

RESULT 15

Q8K397 PRELIMINARY; PRT; 146 AA.
 ID Q8K397
 AC Q8K397
 DT 01-OCT-2002 (T=EMBLrel. 22, Created)
 DT 01-OCT-2002 (T=EMBLrel. 22, Last sequence update)
 DR GO; GO:004869; P:cytosteine protease inhibitor activity; IEA.
 DR InterPro; IPR000010; Cystatin.
 DR Pfam; PF00031; cystatin; 1.
 DR SMART; SM00043; CY; 1.
 FT NON-TER 1 1
 SQ SEQUENCE 146 AA; 16380 MW; 9D77BB9A6063A5C4 CRC64;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Strausberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC021680; AAH27680.1; - (Created)
 DR GO; GO:004869; P:cytosteine protease inhibitor activity; IEA.
 DR InterPro; IPR000010; Cystatin.
 DR Pfam; PF00031; cystatin; 1.
 DR SMART; SM00043; CY; 1.
 FT NON-TER 1 1
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Query Match Score 16.8%; Score 111; DB 11; Length 146;
 Best Local Similarity 30.5%; Pred. No. 0.002;
 Matches 29; Conservative 18; Mismatches 42; Indels 6; Gaps 4;
 DR 20 PTNSPPLLEELTHTTKLNNATNATYFKIDNWKARRVQVAGKRYFIDFVARETTCSKE 79
 DR 40 PTD-PRVQKAQAAVASYNNGSDSIIYFRDTKVIDAKYQLVGIKYLTLDIESTECRKT 98

Qy 80 --SNEEL-TESCETKRLGQ--SLDGNAEYVVWPW 109
 Db 80 --SNEEL-TESCETKRLGQ--SLDGNAEYVVWPW 109

Db 99 RVSGEHMDLTTCPLAAGQQQEKLRCNFELLEVPWK 133
 Search completed: September 24, 2004, 14:10:17
 Job time : 38.424 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 24, 2004, 14:06:08 ; Search time 13.284 Seconds

(without alignments) 890.662 Million cell updates/sec

Title: US-10-661-784-1

Perfect score: 660

Sequence: 1 GKFVQPPTKICVGCPDIP.....YVVPNEKKIYPTVNCGPLGM 123

Scoring table: BLOSUM62

GapOp 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	660	KGHUL1	427	1	KGHUL1	kininogen, LMW pre
2	660	KGHUL1	644	1	KGHUL1	kininogen, HMW pre
3	477	KGBOL1	436	1	KGBOL1	kininogen, LMW I p
4	477	KGBOL1	621	1	KGBOL1	kininogen, HMW I p
5	450	KGBOL2	434	1	KGBOL2	kininogen, HMW II
6	450	KGBOL2	619	1	KGBOL2	K-kininogen, HMW II
7	426	A28055	433	2	A28055	kininogen, HMW I p
8	426	A28055	639	2	A28055	major acute phase T-kininogen, HMW I
9	409	A28055	430	2	A28055	major acute phase T-kininogen, HMW I
10	409	B28055	430	2	B28055	T-kininogen I precur
11	401	KGRTT1	423	1	KGRTT1	cystatin C precursors
12	401	KGRTT1	608	430	KGRTT1	cystatin C precursors
13	136	UDHU	112	1	UDHU	cystatin C precursors
14	133	UDHU	91	2	UDHU	cystatin C precursors
15	133	UDHU	202	91	UDHU	cystatin C precursors
16	130	UDHU	197	127	UDHU	cystatin C precursors
17	129	UDHU	195	120	UDHU	cystatin C - rat
18	128	UDHU	194	111	UDHU	cystatin C - puff ad
19	127.5	UDHU	193	140	UDHU	cystatin C precursors
20	127.5	UDHU	193	146	UDHU	cystatin C precursors
21	125	UDHU	189	141	UDHU	cystatin C precursors
22	118.5	UDCH	180	139	UDCH	cystatin C precursors
23	113.5	UDCH	172	122	UDCH	sarcocystatin A precursors
24	113	UDCH	171	141	UDCH	cystatin S precursors
25	111.5	UDCH	169	111	UDCH	cystatin S chain
26	109.5	UDCH	166	141	UDCH	cystatin S precursors
27	109	UDCH	165	141	UDCH	cystatin S precursors
28	107.5	UDCH	163	132	UDCH	cystatin S precursors
29	107	UDCH	162	132	UDCH	cystatin S precursors

ALIGNMENTS

30	105.5	16.0	162	2	A43428	onchocystatin - ne
31	97.5	14.8	135	2	JC4007	cystatin precursor
32	97	14.7	133	2	JC4536	hypothetical prote
33	95.5	14.5	143	2	T33301	cystatin D precurs
34	95	14.4	142	2	A41742	cystatin-related e
35	93.5	14.2	139	2	A41361	alpha-2-HS-glyco
36	93.5	14.2	135	2	S21094	cystatin - avocado
37	91.5	13.9	100	2	JH0269	cysteine proteins
38	91.5	13.9	135	2	S27239	catuin precursor -
39	90.5	13.7	375	2	A32327	cysteine proteins
40	88.5	13.4	125	2	T00752	cysteine proteins
41	88.5	13.4	134	2	S51828	cysteine proteins
42	88.5	13.4	134	2	JCA882	cystatin - maize
43	85.5	13.0	367	1	W0HJ	alpha-2-HS-glyco
44	85	12.9	199	1	S65071	cystatin - field m
45	84.5	12.8	592	2	T50516	Ca2+ dependent lip

RESULT 1

KGHUL1

kininogen, LMW precursor [validated] - human

N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen

N;Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen

C;Species: Homo sapiens (man)

C;Date: 06-Jul-1982 #sequence-revision 27-Nov-1985 #text-change 08-Dec-2000

C;Accession: A01280; B25277; A27900; A27659; A31905; A34030

R;Ohkubo, I.; Kurachi, K.; Takisawa, T.; Shiokawa, H.; Sasaki, M.

Biochemistry 23, 5691-5697, 1984

A;Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its identi

A;Reference number: A90490; MUID: 85122621; PMID: 6441591

A;Accession: A01280

A;Molecule type: mRNA

A;Residues: 1-427 <OHK>

A;Cross-references: GB:K02566; NID:9177889; PID:AAA35497.1; PMID:9177890

R;Takagaki, Y.; Kitamura, N.; Nakamishi, S.

J. Biol. Chem. 260, 8601-8609, 1985

A;Title: Cloning and sequence analysis of cDNAs for human high molecular weight and low

A;Accession number: A92544; MUID: 85234582; PMID:2989293

A;Accession: B25276

A;Molecule type: mRNA

A;Residue: 1-427 <TAK>

A;Cross-references: GB: M11437; NID:9186751; PID:9386853

R;Hottschied, F.; Kellermann, J.; Hanschen, A.; Rauth, G.; Mueller-Ester, W.

in Kinins IV, part A, Greenbaum, L.M., and Margolis, H.S., eds., pp. 91-95, Plenum, New

A;Title: Amino acid sequence of the light chain of human low molecular mass kininogen.

A;Accession number: A27900

A;Accession: A27900

A;Molecule type: protein

A;Residues: 390-427 <LOT>

R;Mindruo, T.; Carretero, O.A.; Proud, D.; Walz, D.; Sicili, A.G.

Biochem. Biophys. Res. Commun. 152, 519-526, 1988

A;Title: A new kinin moiety in human plasma kininogens.

A;Reference number: A27699; MUID: 88209021; PMID:3365237

A;Accession: A27699

A;Molecule type: protein

A;Residues: 380-389 <MIN>

R;Maeda, H.; Matsumura, Y.; Kato, H.

J. Biol. Chem. 263, 16051-16054, 1988

A;Title: Purification and identification of hydroxyprolyl(3)-bradykinin in ascitic fluid

A;Reference number: A31905; MUID: 89034061; PMID:3182782

A;Accession: A31905

A;Molecule type: protein

A;Residues: 381-389 <MAE>

R;Sasaguri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K.

Biochem. Biophys. Res. Commun. 150, 511-516, 1988

A;Title: Identification of hydroxyproline(3)-lysyl-bradykinin released from human plas

A;Reference number: A34030; MUID: 88106632; PMID:3337729

A;Accession: A34030

A;Molecule type: protein

A;Residues: 380-389 <SA>

R; Kitamura, N.; Kitagawa, H.; Fukushima, D.; Takegaki, Y.; Miyata, T.; Nakaniishi, S. J. Biol. Chem. 260, 8601-8609, 1985
 A; Title: Structural organization of the human kininogen gene and a model for its evolution
 A; Reference number: A93245; MUID:85334583; PMID:2989294
 A; Contents: annotation; gene organization
 R; Pierce, J.V. Ped. Proc. 27, 52-57, 1968
 A; Title: Structural features of plasma kinins and kininogens.
 A; Reference number: A91455; MUID:90255622; PMID:4952632
 A; Contents: annotation; bradykinin
 C; Comment: The LMW kininogen precursor is produced from the same gene as the HMW form (see C;Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of the C;Comment: Bradiokinin, released from kininogen by kallikrein, is a potent vasodilator, i xypoline residue is present in the kininogen prior to the release of bradykinin.
 C; Genetics:
 A; Gene: GDB:KNG
 A; Cross-references: GDB:125256; OMIM:228960
 A; Map position: 3q27-3q27
 C; Superfamily: kininogen; cystatin homology; cysteine proteinase inhibitor; glyc
 C; Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor;
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:1-19-427/Product: LMW prokininogen (kininogen I) #status predicted <MAT>
 F:1-389/90-427/Product: LMW kininogen II #status predicted <MAT2>
 F:1-379/Product: LMW kininogen heavy chain #status predicted <HCH>
 F:1-131/Domain: cystatin homology <CY1>
 F:1-142-253/Domain: cystatin homology <CY2>
 F:1-64-315/Domain: cystatin homology <CY3>
 F:380-389/Product: lysyl-bradykinin (kallidin II) #status experimental <BDY>
 F:381-389/Product: bradykinin (kallidin I) #status experimental <BDY>
 F:190-127/Product: LMW kininogen light chain #status experimental <LCH>
 F:19/Modified site: Pyroglutidone carboxylic acid (Gln) (in mature form) #status Predicted
 F:2-8-107, 83-94-107-126, 142-145, 206-218-229-248, 264-267, 328-340-351-370/Disulfide bonds:
 F:4-169, 205-294/Binding site: carbohydrate (Asn) (covalent) #status Predicted
 F:379-380/Cleavage site: Net-Lys (kallikrein) #status experimental
 F:383/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental
 F:3-39/390/Cleavage site: Arg-Ser (kallikrein) #status experimental
 F:101/Binding site: carbohydrate (Thr) (covalent) #status absent
 Query Match. Score 660; DB 1; Length 427;
 Best Local Similarity 100.0%; Pred. No. 3.3e-55;
 Matches 123; Conservative 0; Mismatches 0; Gaps 0;
 Qy 1. GKDFFQPPTKICVGCPDIPNNSPELTITLTTKLNAAANNATYFKIDDNVKKARVQTY 60
 Db 253. GKDFFQPPTKICVGCPDIPNNSPELTITLTTKLNAAANNATYFKIDDNVKKARVQY 312
 Qy 61 AGKKYFIDFVARETTCSKSNBELTSETRKLQSLDCNAEYVTPWEEKIYPTVNQF 120
 Db 313 AGKKYFIDFVARETTCSKSNBELTSETRKLQSLDCNAEYVTPWEEKIYPTVNQF 372
 Qy 121 LGM 123
 Db 373 LGM 375

RESULT 2

KKHUH1
 Kininogen, HMW precursor [validated] - human
 N; Alternative names: alpha-2-thiol proteinase inhibitor; preprokininogen; prokininogen
 N; Contains: bradykinin (kallidin I); HMW Kininogen I; HMW Kininogen II; low molecular weight
 C; Species: Homo sapiens (man)
 C; Date: 28-May-1986 #sequence revision 28-May-1986 #text change 08-Dec-2000
 C; Accession: A01279; A5276; S32422; A9153; A24871; A277699; A277699; A31905; A34030; S02
 R; Okuhiko, I.; Kachi, K.; Takasawa, T.; Shiokawa, H.; Sasaki, M.
 Biochemistry 23, 5691-5697, 1984
 A; Title: Isolation of human cDNA for alpha-2-thiol proteinase inhibitor and its identification
 A; Reference number: A90490; MUID:85122621; PMID:6441591
 A; Accession: A01279
 A; Molecule type: mRNA
 A; Residues: 1-389 <OHK>
 A; Cross-references: GB:K02566; NID:G177889
 R; Takasaki, Y.; Kitamura, N.; Nakaniishi, S.

KHUUH1
 Kininogen, HMW precursor [validated] - human
 N; Alternative names: alpha-2-thiol proteinase inhibitor; preprokininogen; prokininogen
 N; Contains: bradykinin (kallidin I); HMW Kininogen I; HMW Kininogen II; low molecular weight
 C; Species: Homo sapiens (man)
 C; Date: 28-May-1986 #sequence revision 28-May-1986 #text change 08-Dec-2000
 C; Accession: A01279; A5276; S32422; A9153; A24871; A277699; A277699; A31905; A34030; S02
 R; Rikitomo, H.; Matsumura, Y.; Maeda, H.
 FEBS Lett. 232, 252-254, 1988
 A; Title: Completion of the primary structure of human high-molecular-mass kininogen. The amino acid sequence of the light chain of human high-molecular-mass kininogen. The
 A; Reference number: A24871; MUID:86030270; PMID:4054110
 A; Accession: A91153
 A; Molecule type: protein
 A; Residues: 379-614 <LOT>
 A; Note: The bradykinin sequence preceding the light chain sequence was not determined in
 R; Kellermann, J.; Lotzspeich, F.; Henschien, A.; Mueller-Esterl, W., ed., pp.85-89, Plenum Press, New York
 in Kinins IV, Greenbaum, L.M., and Margolius, H.S.,
 Eur. J. Biochem. 154, 471-478, 1986
 A; Title: Completion of the primary structure of human high-molecular-mass kininogen. The
 A; Reference number: A24871; MUID:86108361; PMID:3484703
 A; Accession: A24871
 A; Molecule type: protein
 A; Residues: 'Z', 20-380 <KEL1>
 A; Note: The bradykinin sequence preceding the light chain sequence was not determined in
 R; Kellermann, J.; Lotzspeich, F.; Henschien, A.; Mueller-Esterl, W., ed., pp.85-89, Plenum Press, New York
 in Kinins IV, Greenbaum, L.M., and Margolius, H.S.,
 Eur. J. Biochem. 154, 471-478, 1986
 A; Title: Amino acid sequence of the light chain of human high-molecular-mass kininogen. The
 A; Reference number: A27899
 A; Accession: A27899
 A; Molecule type: protein
 A; Residues: 379-389 'K', 390-407 'Q', 409-644 <KEL2>
 R; Mindruiu, T.; Carrasco, O.A.; Proust, D.; Walz, D.; Scicli, A.G.
 Biochem. Biophys. Res. Commun. 104, 519-526, 1982
 A; Title: A new kinin moiety in human plasma kininogens.
 A; Reference number: A27699; MUID:88209021; PMID:3365237
 A; Accession: A27699
 A; Molecule type: protein
 A; Residues: 380-389 <MIN>
 R; Sasaguri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K., H.
 J. Biol. Chem. 263, 16051-16054, 1988
 A; Title: Purification and identification of [hydroxyprolyl(3)-lysyl]-bradykinin in ascitic fluid
 A; Reference number: A11905; MUID:89034061; PMID:3182782
 A; Accession: A31905
 A; Molecule type: protein
 A; Residues: 381-389 <KAE>
 R; Sasaguri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K., H.
 Biochem. Biophys. Res. Commun. 150, 511-516, 1988
 A; Title: Human cathepsin B and cysteine proteinase inhibitors (CPIs) in inflammatory and
 A; Reference number: S02482; MUID:89076517; PMID:3224507
 A; Accession: S02482
 A; Molecule type: protein
 A; Residues: 380-389 <SAS>
 R; Lenarcic, B.; Gabrilicic, D.; Rozman, B.; Drobnic-Kosorok, M.; Turk, V.
 Biol. Chem. Hoppe-Seyler 369, 257-261, 1988
 A; Title: Human cathepsin B and cysteine proteinase inhibitors (CPIs) in inflammatory and
 A; Reference number: S02482; MUID:89076517; PMID:3224507
 A; Accession: S02482
 A; Molecule type: protein
 A; Residues: 1-19-192-310-314-381-389 <LEN1>
 R; Rikitomo, H.; Matsumura, Y.; Maeda, H.
 FEBS Lett. 232, 252-254, 1988
 A; Title: Isolation and identification of hydroxycyclopamine analogues of bradykinin in human
 A; Reference number: A61495; PMID:8821189; PMID:3366244
 A; Accession: A61495
 A; Molecule type: protein
 A; Residues: 380-389 <KAT1>
 A; Experimental source: urine

A;Note: this peptide had Pro-383 modified to 4-hydroxyproline
A;Accession: B61495
A;Molecule type: protein
A;Residues: 381-389 <KAT>
A;Experimental source: urine
A;Note: this peptide had Pro-383 modified to 4-hydroxyproline
A;Accession: C61495
A;Molecule type: protein
A;Residues: 380-389 <KAT>
R;Lenerharcic, B.; Krasavcic, M.; Ritonja, A.; Olafsson, I.; Turk, V.
FBS Lett. 207, 211-215, 1991
A;Title: Inactivation of human cystatin C and kininogen by human cathepsin D.
A;Reference number: S14303; MUID:91192133; PMID:201314
A;Accession: S1447
A;Molecule type: protein
A;Residues: 264-359,'N',361-375 <LEN2>
R;Little, S.S.; Johnson, D.A.
Biochem. J. 307, 341-346, 1995
A;Title: Human mast cell tryptase isoforms: separation and examination of substrate-specificity
A;Reference number: S55239; MUID:95251539; PMID:7733867
A;Accession: S55239
A;Molecule type: protein
A;Residues: 450-452,'X',454,'X',456 <LEN>
R;Straczek, J.; Maachi, F.; Le Nguyen, D.; Becchi, M.; Heulin, M.H.; Nabb, P.; Belliveau
FBS Lett. 373, 207-211, 1995
A;Title: Purification from human plasma of a tetrapeptide that potentiates insulin-like
A;Reference number: S68059; MUID:96033974; PMID:7589467
A;Accession: S68059
A;Molecule type: protein
A;Residues: 431-434 <STR>
R;Kitamura, N.; Kitagawa, H.; Fukushima, D.; Takagaki, Y.; Miyata, T.; Nakanishi, S.
J. Biol. Chem. 260, 8610-8617, 1985
A;Title: Structural features of the human kininogen gene and a model for its evolution
A;Content: annotation; gene organization
R;Pierce, J.V.
Fed. Proc. 27, 52-57, 1968
A;Title: Structural features of plasma kinins and kininogens.
A;Reference number: A92515; MUID:92255622; PMID:4952632
A;Content: annotation; bradykinin
C;Comment: The HMW kininogen precursor and the LMW form are produced from the same gene
C;Comment: Kininogen is a cysteine protease inhibitor, takes part in initiation of the
C;Comment: The Glycine/histidine/lysine-rich region of HMW kininogen light chain is important
C;Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, i
C;Genetics:
A;Gene: GDA; KNG
A;Cross-references: GDB:12252566; OMIM: 228960
A;Map position: 3q27.3-q27
A;Intons: 65/3; 102/3; 131/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3
C;Superfamily: kininogen; cystatin homology
C;Keywords: alternative splicing; blood coagulation; cysteine protease inhibitor; dupl
F:1-18/Domain: signal sequence #status experimental <SIG>
F:19-379/Domain: HMW kininogen I (prokininogen) #status experimental <MAN1>
F:19-379/Domain: HMW kininogen II #status experimental <MAN2>
F:19-131/Domain: HMW kininogen heavy chain #status experimental <HCH>
F:142-253/Domain: cystatin homology <CY1>
F:264-375/Domain: cystatin homology <CY2>
F:289/389/Product: lysyl-bradykinin (kallidin II) #status experimental <RBDY>
F:381-389/Product: bradykinin (kallidin I) #status predicted <BDY>
F:389-388/Product: bradykinin I light chain #status predicted <LCH>
F:1-389-436/Product: LMW kininogen I light chain #status experimental <LCH>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F:21-406,82-93,106-125,141-144,205-217,228-247,263-279,350-359,359-368 Disulfide bonds:
F:47, 87, 168, 169, 197, 204/Banding site: carbohydrate (Asn) (covalent) #status predicted
F:378-379/Cleavage site: Met-Lys (kallikrein) #status Predicted
F:382/Modified site: 4-hydroxyproline (Pro) #status Predicted
F:388-389/Cleavage site: Arg-Ser (kallikrein) #status Predicted
Query Match 72.3%: Score 477; DB 1; Length 436;
Best Local Similarity 71.9%; Pred. No. 9.2e-38;
Matches 87; Conservative 14; Mismatches 20; Indels 0; Gaps 0;
Qy 2 KDFVQPTKICVGCPDIPNTSPELEBLTITKNAENNATFYKIDNTYKARVQVA 61
Db 253 KDFVQPTKICVGCPDIPNTSPELEBLTITKNAENNATFYKIDNTYKARVQVA 312
Qy 62 GKRYFIDFVARETTCSKESNEELTESCETKLQGSDLDCNAEVYVPEWEKKIYPTVCQPL 121
Db 313 GLKYSIVFIARETTCSKGSNEELTKSCSINHGQILHCDANVVVPEWEKKIYPTVCQPL 372
Qy 122 G 122
Db 373 G 373

P;169,205-294/Banding site: carbohydrate (Asn) (covalent) #status absent
P;379-380/Cleavage site: Met-Lys (kallikrein) #status experimental
P;383/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental
P;389-390/Cleavage site: Arg-Ser (kallikrein) #status experimental
P;401-533,542,546,557,571,593,628/Binding site: carbohydrate (Thr) (covalent) #status ex
P;577/Binding site: carbohydrate (Ser) (covalent) #status experimental

RESULT 4

RgBOH1
kininogen, HMW I precursor - bovine
N;Alternative names: alpha-2-thiol proteinase inhibitor; preprokininogen
N;Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen
C;Date: 14-Nov-1983 #sequence revision 14-Nov-1983 #text_change 22-Jun-1999
C;Accession: A01281; A91938; A91939; A91938; A91939
R;Kitamura, R.; Takasaki, Y.; Furuto, S.; Tanaka, T.; Nawa, H.; Nakanishi, S.
Nature 305, 545-549, 1983
A;Title: A single gene for bovine high molecular weight and low molecular weight kininogen
A;Reference number: A93317; MUID:8401406; PMID:6571699
A;Accession: A01281
A;Molecule type: mRNA
A;Cross-references: GB:V01491; GB:K01757; NID:9491; PIDN:CAA24735.1; PID:9492
R;Kato, H.; Nagasawa, S.; Suzuki, T.
J. Biochem. 67, 313-322, 1970
A;Title: Studies on the structure of bovine kininogen: cleavages of disulfide bonds and
A;Reference number: A91923; MUID:70180420; PMID:4986212
A;Accession: A91923
A;Molecule type: protein
A;Residues: 378-393 <KAT>
R;Han, Y.N.; Komiyama, M.; Iwanaga, S.; Suzuki, T.
J. Biochem. 77, 55-68, 1975
A;Title: Studies on the primary structure of bovine high-molecular-weight kininogen. Ami
A;Reference number: A91938; MUID:75170265; PMID:1169237
A;Accession: A91938
A;Molecule type: protein
A;Residues: 458-498 <HAN>
R;Sueyoshi, T.; Miyata, T.; Hashimoto, N.; Kato, H.; Miyata, T.; Iwanaga, S.
J. Biol. Chem. 262, 2762-2768, 1987
A;Title: Bovine high molecular weight kininogen. The amino acid sequence, positions of c
A;Reference number: A92627; MUID:87137530; PMID:35462295
A;Accession: A92627
A;Molecule type: protein
A;Residues: 'Z', '20-123', 'I', '125-127', 'I', '129-378 <SUB>
R;Dottelpeich, F.; Kellermann, J.; Henschen, A.; Poertsch, B.; Muller-Esterl, W.
Eur. J. Biochem. 152, 307-314, 1985
A;Title: The amino acid sequence of the light chain of human high-molecular-mass kininog
A;Reference number: A91153; MUID:86030270; PMID:4054110
A;Contents: annotation; bovine cleavage sites; bovine carbohydrate binding sites
R;Sueyoshi, T.; Miyata, T.; Kato, H.; Iwanaga, S.
Seikagaku 56, 809, 1994
A;Title: Disulfide bonds in bovine HMW kininogens.
A;Contents: annotation; bovine HMW kininogens.
A;Note: article in Japanese
A;Accession: A934300
A;Contents: annotation; disulfide bonds
C;Comment: The HMW kininogen precursor is produced from the same gene as the LMW form as the
C;Comment: Kininogen is a cysteine proteinase inhibitor. Takes part in initiation of the
C;Comment: The glycine/histidine/lysine-rich region of HMW kininogen light chain is impo
C;Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, i
xyproline residue is present in the kininogen prior to the release of bradykinin.
C;Superfamily: kininogen; cystatin homology
C;Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; dupl
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-921/Product: HMW prokininogen I #status predicted <MAT>
F:19-379/Domain: cystatin homology <CY1>
F:19-130/Domain: cystatin homology <CY1>
F:141-252/Domain: cystatin homology <CY2>
F:251-372/Domain: cystatin homology <CY2>
F:377-386/Product: lysyl-bradykinin (kallidin II) #status predicted <BDY>
F:378-386/Product: bradykinin (kallidin II) #status predicted <BDY>
F:387-394/Product: LMW kininogen light chain #status predicted <LCH>
F:39/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F:21-404, 82-3106-125, 141-144, 205-217, 228-247, 261-264, 325-337, 348-367/Disulfide bonds:
F:47, 87, 168, 169, 197, 204, 280/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:316-377/Cleavage site: Met-Lys (kallikrein) #status predicted
F:380/Modified site: 4-hydroxyproline (Pro) #status predicted
F:386-387/Cleavage site: Arg-Ser (kallikrein) #status predicted

RESULT 5

KGBOL2
kininogen, LMW II precursor - bovine
N;Alternative names: alpha-2-thiol proteinase inhibitor; preprokininogen
N;Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen
C;Species: Bos Primigenius taurus (cattle)
C;Accession: A01284
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983
R;Nawa, H.; Kitamura, N.; Hirose, T.; Asai, M.; Inayama, S.; Nakanishi, S.
Proc. Natl. Acad. Sci. U.S.A. 80, 90-94, 1983
A;Title: Primary structures of bovine liver low molecular weight kininogen precursors and
A;Reference number: A93984; MUID:8317855; PMID:6572010
A;Accession: A01284
A;Molecule type: mRNA
A;Residues: 1-434 <NAW>
A;Cross-references: GB:V00427; GB:J00011; NID:9489; PID:CAA23710.1; PID:G190
C;Comment: The LMW kininogen precursor is produced from the same gene as the HMW form as
the C;Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of the
C;Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, i
xyproline residue is present in the kininogen prior to the release of bradykinin.
C;Superfamily: kininogen; cystatin homology
C;Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; glycc
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-434/Product: LMW kininogen II #status predicted <MAT>
F:19-377/Domain: cystatin homology <CY1>
F:19-130/Domain: cystatin homology <CY1>
F:141-252/Domain: cystatin homology <CY2>
F:251-372/Domain: cystatin homology <CY2>
F:377-386/Product: lysyl-bradykinin (kallidin II) #status predicted <BDY>
F:378-386/Product: bradykinin (kallidin II) #status predicted <BDY>
F:387-394/Product: LMW kininogen light chain #status predicted <LCH>
F:39/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F:21-404, 82-3106-125, 141-144, 205-217, 228-247, 261-264, 325-337, 348-367/Disulfide bonds:
F:47, 87, 168, 169, 197, 204, 280/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:316-377/Cleavage site: Met-Lys (kallikrein) #status predicted
F:380/Modified site: 4-hydroxyproline (Pro) #status predicted
F:386-387/Cleavage site: Arg-Ser (kallikrein) #status predicted

F:398-406, 512/Binding site: carbohydrate (Ser) (covalent) #status experimental ext
F:399-400, 520, 524, 536, 548, 553-570/Binding site: carbohydrate (Thr) (covalent) #status experimental ext
F:498-499/Cleavage site: Arg-Inr (kallikrein) #status experimental

Query	Match	Score	DB	Length
QY	2 KDPVQPKICVGCPDPINTSPPELTITKNAENNAFTYFKIDNVKARVQVVA	72.3%	1	621;
Db	253 KDPVQPKICVGCPDPINTSPPELTITKNAENNAFTYFKIDNVKARVQVVA	71.9%	1	620; Indels 0;
QY	62 GCKYFIDFDEVARETCSKESNEELTESETKLGSQDNCNAEVVYVWEKKIYPTVNQPL	Score 477;	1	121;
Db	313 GLKYSIVPIARETCSKGSNEBLTKSCENIHQILHCDANVVVPEEKVYPTVNQPL	Conservative 14;	1	372
QY	122 G 122	Mismatches 20;	1	
Db	373 G 373	Indels 0;	1	

Db 370 LG 371

RESULT 6

KGDB012 kininogen, HMW II precursor - bovine

N; Alternate names: alpha-2-thiol proteinase inhibitor; prekininogen

N; Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen

C; Species: Bos primigenius taurus (cattle)

C; Date: 14-Nov-1983 #sequence revision 14-Nov-1983 #text_change 22-Jun-1999

R; Kitamura, N.; Takagaki, Y.; Furuto, S.; Tanaka, T.; Nakanishi, S.

R; Title: A single gene for bovine high molecular weight kininogen

A; Reference number: A93317; MUID:6571699

A; Accession: A01282

A; Molecule type: mRNA

A; Residues: 1-619 <KIT>

A; Cross-references: GB:V01492; GB:K01758; MJD:9493; PID:CAA24736.1; PID:g494

R; Kato, H.; Nagasawa, S.; Suzuki, T.

J; Biochem, 67, 313-323, 1970

A; Title: Studies on the structure of bovine kininogen: cleavages of disulfide bonds and

A; Reference number: A91933; MUID:7018020; PMID:4986212

A; Accession: A91923

A; Molecule type: protein

A; Residues: 376-391 <KAT>

R; Han, Y.N.; Kato, H.; Iwanaga, S.; Suzuki, T.

J; Biochem, 79, 1201-1222, 1976

A; Title: Primary structure of bovine plasma high-molecular-weight kininogen. The amino acid sequence of bovine kininogen

A; Reference number: A91941; MUID:76260155; PMID:956151

A; Accession: A91941

A; Molecule type: protein

A; Residues: 387-455 <HAN>

A; Note: 398-Pro, 401-Val, and 455-Lys were also found

R; Han, Y.N.; Komiya, M.; Iwanaga, S.; Suzuki, T.

J; Biochem, 77, 55-68, 1975

A; Title: Studies on the primary structure of bovine high-molecular-weight kininogen. Ami

A; Reference number: A91938; MUID:75170265; PMID:1169237

A; Accession: A91938

A; Molecule type: protein

A; Residues: 456-496 <HA2>

R; Sueyoshi, T.; Miyata, T.; Hashimoto, N.; Kato, H.; Miyata, T.; Iwanaga, S.

J; Biol. Chem., 262, 2768-2779, 1987

A; Title: Bovine high molecular weight kininogen. The amino acid sequence, positions of C

A; Content: annotation; bovine cleavage sites; bovine carbohydrate binding sites

R; Sueyoshi, T.; Miyata, T.; Kato, H.; Iwanaga, S.

Seikaku, 56, 808, 1984

A; Title: Disulfide bonds in bovine HMW kininogens.

A; Reference number: A94300

A; Contents: annotation; disulfide bonds

A; Note: article in Japanese

C; Comment: The HMW kininogen precursor is produced from the same gene as the LMW form as

C; Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of the light chain of HMW kininogen, released from kininogen by kallikrein, is a potent vasodilator, i

C; Superfamily: Kininogen; cystatin homology; cysteine proteinase inhibitor; dup1

C; Comment: The glycine/histidine/lysine-rich region of HMW kininogen II heavy chain is impo

C; Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, i

C; Superfamily: Kininogen; cystatin homology <CY1>

C; Keywords: alternative splicing; blood coagulation; cysteine proteinase

C; Comment: Bradykinin is a cysteine proteinase inhibitor, takes part in initiation of the

C; Comment: The glycine/histidine/lysine-rich region of HMW kininogen II heavy chain is impo

C; Superfamily: Kininogen; cystatin homology <CY1>

C; Superfamily: Kininogen; cystatin homology <CY2>

C; Superfamily: Kininogen; cystatin homology <CY3>

C; Superfamily: Kininogen; cystatin homology <CY4>

P;378-386/Product: bradykinin (kallidin I) #status experimental <BDY>
 P;387-619/Product: HMW kininogen II light chain #status experimental <LCH>
 P;418-588/Region: glycine/histidine/lysine-rich
 P;19/Modified site: Pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental
 P;27-59 82-93 106-115 141-144 205-217 228-247 261-264 325-337 348-367/Disulfide bonds:
 P;47/Binding site: carbohydrate (Asn) (covalent) #status absent
 P;136 168-169 204-280/Binding site: carbohydrate (Asn) (covalent) #status experimental
 P;197/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental
 P;176-177/Cleavage site: Met-Lys (kallikrein) #status Predicted
 P;380/Modified site: 4-hydroxyproline (Pro) #status Predicted
 P;386-387/Cleavage site: Arg-Ser (kallikrein) #status experimental
 P;396,400,404,510/Binding site: carbohydrate (Ser) (covalent) #status experimental
 P;397,398,518,522,534,546,551,568/Binding site: carbohydrate (Thr) (covalent) #status ex
 P;496-497/Cleavage site: Arg-Thr (kallikrein) #status experimental

Query Match Score 68.2%; DB 1; Length 619;
 Best Local Similarity 68.9%; Pred. No. 5.1e-15;
 Matches 84; Conservative 14; Mismatches 22; Indels 2; Gaps 1;
 QY 1 GKDFFQPPTKICVGCPRIDPTNSPELEBLTHTITKNAENNAATTYFKIDNVKAKAVQQV 60
 Db 252 GEDELL--PPMVCGCPKPPIPVDSPDPEALHNTIAKLNAAHDGTFPKIDTVKKAKVQVV 309
 QY 61 AGKKFIDFVARETTCSKESNEELTESETKRLGQSLDCNAEVYYWEKTYPTYNQCP 120
 Db 310 GGKRYSTVFIARETTCSKGSNBELTKSCEINIHQQLHCDANVIVVWEKTYPTYNQCP 369
 QY 121 LG 122
 Db 370 LG 371.

RESULT 7
 A2055
 K;Kininogen, LMW I precursor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 20-Jun-1989 #sequence_revision 20-Jun-1989 #text_change 15-Nov-1996
 C;Accession: A28055
 R;Puruto-Kato, S.; Matsumoto, A.; Kitamura, N.; Nakanishi, S.
 J; Biol. Chem., 260, 12054-12059, 1985
 A;Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin and inhibitor. A;Reference number: A92496; MUID:86008264; PMID:2413018
 A;Accession: A28055
 A;Molecule type: mRNA
 A;Residues: 1-433 <FUR>
 C;Superfamily: cystatin homology
 C;Keywords: alternative splicing
 C;Domain: signal sequence #status predicted <SIG>
 P;19-433/Product: K-kininogen, LMW I #status predicted <MAT>
 P;19-131/Domain: cystatin homology <CY1>
 P;142-255/Domain: cystatin homology <CY2>
 P;254-379/Domain: cystatin homology <CY3>
 Query Match Score 64.5%; DB 2; Length 433;
 Best Local Similarity 65.0%; Pred. No. 6.e-33;
 Matches 80; Conservative 14; Mismatches 29; Indels 0; Gaps 0;
 QY 1 GKDFFQPPTKICVGCPRIDPTNSPELEBLTHTITKNAENNAATTYFKIDNVKAKAVQQV 60
 Db 253 GDDLFELLPEDCGCPKPPIPVDSPDPEALHNTIAKLNAAHDGTFPKIDTVKKAKVQVV 312
 QY 61 AGKKFIDFVARETTCSKESNEELTESETKRLGQSLDCNAEVYYWEKTYPTYNQCP 120
 Db 313 AGTKVIEETRKCSKGSNBELTKSCEINIHQQLHCDANVIVVWEKTYPTYNQCP 372
 QY 121 LGM 123
 Db 373 LDM 375

RESULT 8

P;377-386/Product: lysyl-bradykinin (kallidin II) #status experimental <BDY>

Qy 121 LGM 123
 Db 372 LDM 374

RESULT 10

B28055 T-kininogen, LMW II precursor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 20-Jun-1989 #sequence_revision 08-Mar-1989 #text_change 15-Nov-1996
 C;Accession: B25486
 R;Kitajawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.
 J. Biol. Chem. 262, 2190-2198, 1987
 A;Title: Differing expression patterns and evolution of the rat kininogen gene family.
 A;Reference number: A92625; PMID:87137443; MUID:30290688
 A;Accession: A25486
 A;Molecule type: mRNA
 A;Residues: 1-639 <KMT>
 A;Note: the authors translated the codon CAA for residue 347 as Asn
 C;Superfamily: kininogen; cystatin homology
 C;Keywords: alternative splicing
 F;1-18/Domain: signal sequence #status predicted <SIG>
 F;1-19-131/Domain: cystatin homology <CY1>
 F;142-253/Domain: cystatin homology <CY2>
 F;264-375/Domain: cystatin homology <CY3>

Query Match 64.5% Score 426; DB: 2; Length 639;
 Best Local Similarity 65.0%; Pred. No. 1e-32; Indels 0; Gaps 0;
 Matches 80; Conservative 14; Mismatches 29; Indels 0; Gaps 0;

Qy 1 GKDFFQPPTKICVGCPDDIPTNSPELETTITKLNAENNTYFKIDNVKARVQVV 60
 Db 253 GDDLFELLEDPGCPNPKIVPDSPELKEAHLGHSTIAQLNAENNHTYFKIDTVKATSQVV 312

Qy 61 AGKKYFIDFVARETTCSKESNEELTSCETKLGSQSLDNCAEVYYTPWEEKTYPTVNQCP 120
 Db 313 AGTKYVIEIFIARETTCSKESNEELTACETKLGSQSLDNCAEVYYTPWENKVPVKCRV 372

Qy 121 LGM 123
 Db 373 LDM 375

RESULT 9
 major acute phase alpha-1 protein (version 2) - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Accession: 19-May-1989 #sequence_revision 19-May-1989 #text_change 20-Aug-1999
 R;Anderson, K.P.; Heath, B.C.
 J. Biol. Chem. 260, 12065-12071, 1985
 A;Title: The relationship between rat major acute phase protein and the kininogens.
 A;Reference number: A23897; PMID:86008266; MUID:2413019
 A;Accession: A23897
 A;Molecule type: protein
 A;Residues: 1-14 <AND1>
 A;Accession: B23897
 A;Molecule type: mRNA
 A;Residues: 5-430 <AND2>
 A;Cross-references: GB:MM11661; NID:9205307; PIDN:AAA11570.1; PID:9205308
 A;Note: the authors translated the codon CTC for residue 410 as Arg, CTA for residue 419
 F;19-130/Domain: cystatin homology
 F;141-252/Domain: cystatin homology <CY1>
 F;263-374/Domain: cystatin homology <CY2>

Query Match 62.0% Score 409; DB: 2; Length 430;
 Best Local Similarity 61.8%; Pred. No. 2.7e-12; Indels 0; Gaps 0;
 Matches 76; Conservative 15; Mismatches 32; Indels 0; Gaps 0;

Qy 1 GKDFFQPPTKICVGCPDDIPTNSPELETTITKLNAENNTYFKIDNVKARVQVV 60
 Db 252 GDDLFELLEDPGCPNPKIVPDSPELKEAHLGHSTIAQLNAENNHTYFKIDTVKATSQVV 311

Qy 61 AGKKYFIDFVARETTCSKESNEELTSCETKLGSQSLDNCAEVYYTPWEEKTYPTVNQCP 120
 Db 312 AGTKYVIEIFIARETTCSKESNEELTACETKLGSQSLDNCAEVYYTPWENKVPVKCRQAA 371

Qy 121 LGM 123
 Db 372 LDM 374

RESULT 11

Qy 1 GKDFFQPPTKICVGCPDDIPTNSPELETTITKLNAENNTYFKIDNVKARVQVV 60
 Db 252 GDDLFELLEDPGCPNPKIVPDSPELKEAHLGHSTIAQLNAENNHTYFKIDTVKATSQVV 311

C;Species: Rattus norvegicus (Norway rat)
 C;Accession: Nov-1985 #sequence_revision 27-Nov-1985
 C;Date: 27-Nov-1985 #text_change 12-Apr-1996
 R;Cole, T.; Inglis, A.S.; Roxburgh, C.M.; Howlett, G.J.; Schreiber, G.

FEBS Lett. 182, 57-61, 1985
 A;Title: Major acute phase alpha1-protein of the rat is homologous to bovine kininogen a
 r.
 A;Reference number: A01285; MUID:85127561; PMID:2578392

A;Accession: A01285

A;Molecule type: mRNA

A;Residues: 1-423 <COL>

C;Comment: This plasma glycoprotein inhibits cysteine proteinases. During acute inflamma-

r.
 C;Superfamily: kininogen; cystatin homology

C;Keywords: bradykinin; cysteine proteinase inhibitor; duplication; glycoprotein; inflam-

r;I-11/Domain: signal sequence (fragment) #status predicted <SG>

F;I-12-123/Domain: major acute phase alpha-1 protein #status predicted <MAT>

F;I-134-45/Domain: cystatin homology <CRY1>

F;I-371-379/Domain: cystatin homology <CRY3>

F;I-12/Modified site: pyrrolidone carboxylic acid (Asn) (covalent) #status Predicted

F;I-16,19/Binding site: carboxylic acid (Gln) (in mature form) #status Predicted

Query Match Score 402; DB 1; Length 423;

Best Local Similarity 61.8%; Pred. No. 1.2e-30;

Matches 76; Conservative 33; Indels 0; Gaps 0;

Matches 76/ Binding site: carboxylic acid (Asn) #status Predicted

Qy 1 GAKKFIDYFVARETCSKESNEELTESCETKKGSLDNLNAEVTVVPMKKPTVNCQ 60

Db 245 GDDLFELLPKNCRGCPREIPIVDSPLKEALGHSTARLNQHNFYFKIDTVKATSOV 304

Qy 61 AGKKYFIDYFVARETCSKESNEELTESCETKKGSLDNLNAEVTVVPMKKPTVNCQ 120

Db 305 AGVIVIEFARETCSKESNEELTESCETKKGSLDNLNAEVTVVPMKKPTVNCQ 364

Qy 121 LGM 123

Db 365 LDM 367

RESULT 12

T-kininogen I precursor - rat

N;Alternate names: 73k protein; LMW kininogen T-I

N;Contains: bradykinin; T-kinin

C;Species: Rattus norvegicus (Norway rat)

C;Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #ext change 22-Jun-1999

C;Accession: A01286; D25486; A28548; P0193; JQ0027; PMID:3029068

R;Furukawa, S.; Matsumoto, A.; Kitamura, N.; Nakaniishi, S.

J. Biol. Chem. 260, 12054-12059, 1985

A;Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin and

nakinin.

A;Reference number: A92436; MUID:85008264; PMID:2413018

A;Accession: A01286

A;Molecule type: mRNA

A;Residues: 1-430 <PUR>

R;Kitagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakaniishi, S.

J. Biol. Chem. 262, 2190-2198, 1987

A;Title: Differing expression patterns and evolution of the rat kininogen gene family.

A;Reference number: A92625; MUID:87137443; PMID:3029068

A;Molecule type: DNA

A;Residues: 375-430 <KIT>

R;Enjoji, K.; Kato, H.; Hayashi, I.; Ohishi, S.; Iwanaga, S.

J. Biol. Chem. 263, 973-979, 1988

A;Title: Purification and characterization of rat T-kininogens isolated from plasma of a

A;Reference number: A92729; MUID:88087226; PMID:3121623

A;Accession: A28526

A;Molecule type: protein

R;Kanda, S.; Sugiyama, K.; Takahashi, M.; Shumiya, S.; Tomino, S.; Nagase, S.

Jpn. J. Cancer Res. 81, 63-68, 1990

A;Title: Identification of a protein increasing in serum of Nagase analbuminemic rats be-

A;Reference number: PL0193; MUID:90216390; PMID:2108948

A;Accession: PL0193

A;Molecule type: mRNA

A;Residues: 330-420 'R' 422-429 'P' <KAN>

R;Anderson, K.P.; Croyle, M.L.; Lingrel, J.B.

Gene 81, 119-128, 1993

A;Title: Primary structure of a gene encoding rat T-kininogen.

A;Reference number: JQ0027; MUID:90034122; PMID:2806908

A;Accession: JQ0027

A;Molecule type: DNA

A;Residues: 1-60 'E' 62-113 'R' 115-165 'F' 167-178 'TKI' 182-211 'F' 213-256 'S' 258-385

A;Experimental source: strain Sprague-Dawley

R;Kageyama, R.; Kitamura, N.; Ohkubo, H.; Nakaniishi, S.

J. Biol. Chem. 262, 2345-2351, 1987

A;Title: Differential utilization of homologous transcription initiation sites of rat K and

A;Reference number: A25488; MUID:3018598

A;Accession: A25488

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-48 <KAG>

A;Cross-references: GB:MI4356; NID:9205090; PIDN:AAA41492-1; PMID:9205091

R;Enjoji, K.; Kato, H.; Hayashi, I.; Ohishi, S.; Iwanaga, S.

J. Biol. Chem. 263, 965-972, 1988

A;Title: Purification and characterization of two kinds of low molecular weight kininogen

A;Reference number: A28525; MUID:88087225; PMID:3335530

A;Accession: A28525

A;Molecule type: Protein

A;Residues: 340-430 <SIE>

A;Experimental source: clone PG317

C;Comment: At least three types of LMW kininogen precursors are present in rat plasma, t-

ceding bradykinin.

C;Comment: The T-kininogens are produced in response to an inflammatory stimulant.

C;Genetics:

A;Introns: 65/3; 102/3; 130/1; 130/2; 223/2; 252/1; 309/3; 345/3; 374/3; 398/3

A;Introms: 65/3; 102/3; 130/1; 130/2; 223/2; 252/1; 309/3; 345/3; 374/3; 398/3

A;Comments: At least three types of LMW kininogen precursors are present in rat plasma, t-

ceding bradykinin.

C;Comment: The T-kininogens contain T-kinin (1-S-bradykinin), a novel kinin isolated after t-

hird of an Arg or Lys, it is probably not released from its precursor by either tissue or p-

eceding bradykinin.

C;Genetics:

A;Introms: 65/3; 102/3; 130/1; 130/2; 223/2; 252/1; 309/3; 345/3; 374/3; 398/3

A;Introms: 65/3; 102/3; 130/1; 130/2; 223/2; 252/1; 309/3; 345/3; 374/3; 398/3

A;Comments: The T-kininogens contain T-kinin (1-S-bradykinin), a novel kinin isolated after t-

hird of an Arg or Lys, it is probably not released from its precursor by either tissue or p-

eceding bradykinin.

C;Keywords: acute phase; bradykinin; cysteatin homology

C;Keywords: kinase; cysteine proteinase inhibitor; duplication; glycoprotein

C;Keywords: acute phase; bradykinin; cysteatin homology

C;Keywords: kinase; cysteine proteinase inhibitor; duplication; glycoprotein

C;Keywords: acute phase; bradykinin; cysteatin homology

C;Keywords: kinase; cysteine proteinase inhibitor; duplication; glycoprotein

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C;Keywords: kinase; cysteine proteinase inhibitor; duplication; glycoprotein

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C;Keywords: kinase; cysteine proteinase inhibitor; duplication; glycoprotein

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C;Keywords: kinase; cysteine proteinase inhibitor; duplication; glycoprotein

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C;Keywords: kinase; cysteine proteinase inhibitor; duplication; glycoprotein

C;Keywords: acute phase; bradykinin; cysteatin homology

C;Keywords: kinase; cysteine proteinase inhibitor; duplication; glycoprotein

C;Keywords: acute phase; bradykinin; cysteatin homology

C;Keywords: kinase; cysteine proteinase inhibitor; duplication; glycoprotein

C;Keywords: acute phase; bradykinin; cysteatin homology

C;Keywords: kinase; cysteine proteinase inhibitor; duplication; glycoprotein

C;Keywords: acute phase; bradykinin; cysteatin homology

C;Keywords: kinase; cysteine proteinase inhibitor; duplication; glycoprotein

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C;Keywords: kinase; cysteine proteinase inhibitor; duplication; glycoprotein

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C;Keywords: kinase; cysteine proteinase inhibitor; duplication; glycoprotein

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C;Keywords: kinase; cysteine proteinase inhibitor; duplication; glycoprotein

C;Keywords: acute phase; bradykinin; cysteatin homology

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C;Keywords: kinase; cysteine proteinase inhibitor; duplication; glycoprotein

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C;Keywords: kinase; cysteine proteinase inhibitor; duplication; glycoprotein

C;Keywords: acute phase; bradykinin; cysteatin homology

C;Keywords: kinase; cysteine proteinase inhibitor; duplication; glycoprotein

C;Keywords: acute phase; bradykinin; cysteatin homology

C;Keywords: kinase; cysteine proteinase inhibitor; duplication; glycoprotein

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C;Keywords: kinase; cysteine proteinase inhibitor; duplication; glycoprotein

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C;Keywords: acute phase; bradykinin; cysteatin homology

C;Keywords: kinase; cysteine proteinase inhibitor; duplication; glycoprotein

C;Keywords: acute phase; bradykinin; cysteatin homology

C;Keywords: kinase; cysteine proteinase inhibitor; duplication; glycoprotein

C;Keywords: acute phase; bradykinin; cysteatin

C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Feb-1986 #sequence_revision 28-Feb-1986 #text_change 06-Dec-1996
C;Accession: A01271
R:Hirado, M.;Tsunasawa, S.; Sekiyama, F.; Ninobe, M.; Fujii, S.
A;Title: Complete amino acid sequence of bovine colostrum low-M-r cysteine proteinase inhibitor
A;Reference number: A01271; MUID:85231205; PMID:3891407
A;Accession: A01271
A;Molecule type: protein
A;Residues: 1-112 <HTR>
C;Keywords: cystatin; cystatin homology
C;Superfamily: colostrum; cysteine proteinase inhibitor
F:2-112/Domain: cystatin homology <CYS>
F:48-52/Region: inhibitory #status predicted
F:66-76/90-110/Disulfide bonds: #status predicted

Query Match 20.6%; Score 136; DB 1; Length 112;
Best Local Similarity 30.6%; Pred. No. 6.4e-06;
Matches 34; Conservative 22; Mismatches 31; Indels 24; Gaps 5;
Qy 22 NSPELEETLTHPTKNAENNATFYKIDNYKARVQVVAKKRYFILDFTYRETTCSKEEN 81
Db 12 NEEGVQALSAFVAYEENFKRSNDAYQSRVVTYRARKQVVSQMMNYTDVEGLRTCTK-S 69

Query Match 20.6%; Score 136; DB 1; Length 112;
Best Local Similarity 30.6%; Pred. No. 6.4e-06;
Matches 34; Conservative 22; Mismatches 31; Indels 24; Gaps 5;
Qy 82 EETKLGOSLDNAEYTVVPPWEEKIYPTVN----CQ 119
Db 70 QANLDSCPPHNQPHLKREKL----CSFQVTVVPMNN---TINLVKFSSCQ 111

RESULT 14
S68034
T-kininogen (clone pSG22) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 07-May-1999
C;Accession: S68034
R;Sierra, F.; Walter, R.; Vautravers, P.; Guigoz, Y.
Arch. Biochem. Biophys. 322, 333-338, 1995
A;Title: Identification of several isoforms of T-kininogen expressed in the liver of agouti
A;Reference number: S68034; MUID:96032652; PMID:7574705
A;Accession: S68034
A;Molecule type: mRNA
A;Residues: 1-91 <SIE>
A;Experimental source: liver
C;Superfamily: kininogen; cystatin homology
C;Keywords: alternative splicing; cysteine proteinase inhibitor; plasma

Query Match 20.2%; Score 133; DB 2; Length 91;
Best Local Similarity 68.6%; Pred. No. 9.8e-06;
Matches 24; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
Qy 89 ETKLGOSLDNAEYTVVPPWEEKIYPTVNCPGLM 123
Db 1 ETKHLGSILNCNANVYMRPWENKVYPTVRQALDM 35

RESULT 15
S68035
T-kininogen (clone pSG17) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 07-May-1999
C;Accession: S68035
R;Sierra, F.; Walter, R.; Vautravers, P.; Guigoz, Y.
Arch. Biochem. Biophys. 322, 333-338, 1995
A;Title: Identification of several isoforms of T-kininogen expressed in the liver of agouti
A;Reference number: S68034; MUID:96032652; PMID:7574705
A;Accession: S68035
A;Molecule type: mRNA
A;Residues: 1-91 <SIB>
A;Experimental source: liver
C;Superfamily: kininogen; cystatin homology
C;Keywords: alternative splicing; cysteine proteinase inhibitor; plasma

Query Match 20.2%; Score 133; DB 2; Length 91;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 24, 2004, 14:08:41 ; Search time 43.296 Seconds

(without alignments)

913.519 Million cell updates/sec

Title: US-10-661-784-1

Perfect score: 660

Sequence: 1 GxDFQPPTKICVGCPRDIP.....YVVPWEEKIPTVNCQQPLGM 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1349238 seqs, 32155718 residues

Total number of hits satisfying chosen parameters: 1349238

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database :

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Published Applications AA:*
1: /cgns_6/_pcodata/1/pubpaas/US07_PUBCOMB.pep:*
2: /cgns_6/_pcodata/1/pubpaas/PCT_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	660	100.0	390	15 US-10-661-784-1	Sequence 82, App1
2	660	100.0	398	15 US-10-162-335-82	Sequence 70, App1
3	660	100.0	427	10 US-09-919-039-79	Sequence 29, App1
4	660	100.0	615	15 US-10-162-335-72	Sequence 72, App1
5	660	100.0	644	15 US-10-162-335-74	Sequence 74, App1
6	660	100.0	644	15 US-10-162-335-84	Sequence 84, App1
7	60.9	402	424	14 US-10-316-53-217	Sequence 217, App1
8	40.1	60.8	430	14 US-10-316-233-215	Sequence 215, App1
9	16.9	25.6	178	9 US-09-969-834-1	Sequence 1, App1
10	16.5	25.1	145	14 US-10-329-428-2	Sequence 2, App1
11	16.5	25.1	167	10 US-09-746-733-197	Sequence 197, App
12	138.5	21.0	121	9 US-09-775-932-14	Sequence 14, App1
13	138.5	21.0	128	9 US-09-775-932-12	Sequence 12, App1
14	138.5	21.0	149	9 US-09-940-497-2	Sequence 2, App1
15	13.6	20.6	112	8 US-08-849-303-16	Sequence 16, App1
					Sequence 2, App1
					Sequence 19, App1
					Sequence 19, App1
					Sequence 46, App1
					Sequence 48, App1
					Sequence 82, App1
					Sequence 86, App1
					Sequence 86, App1
					Sequence 78, App1
					Sequence 80, App1
					Sequence 93, App1
					Sequence 18, App1
					Sequence 17, App1
					Sequence 3, App1
					Sequence 3, App1
					Sequence 3, App1
					Sequence 47, App1
					Sequence 17, App1
					Sequence 1, App1
					Sequence 4, App1
					Sequence 2, App1
					Sequence 8, App1
					Sequence 24, App1

ALIGNMENTS

RESULT 1	US-10-162-335-82	; Sequence 82, Application US/10162335
		; Publication No. US2004009480A1
		; GENERAL INFORMATION:
		; APPLICANT: Anderson, David W.
		; APPLICANT: Baumgartner, Jason C.
		; APPLICANT: Boldog, Ferenc L.
		; APPLICANT: Casman, Stacie J.
		; APPLICANT: Edinger, Shlomit R.
		; APPLICANT: Ganguli, Bahaa A.
		; APPLICANT: Gerlach, Valerie
		; APPLICANT: Gormani, Linda
		; APPLICANT: Guo, Xiaojia (Sasha)
		; APPLICANT: Hjalt, Tord
		; APPLICANT: Keruda, Ramesh
		; APPLICANT: Li, Li
		; APPLICANT: MacDougall, John R.
		; APPLICANT: Malyantov, Uriel M.
		; APPLICANT: Millet, Isabelle
		; APPLICANT: Padigaru, Muralidhara
		; APPLICANT: Pattarajan, Meera
		; APPLICANT: Pena, Carol E. A.
		; APPLICANT: Rastelli, Luca
		; APPLICANT: Shimkets, Richard A.
		; APPLICANT: Spivak, Kimberly A.
		; APPLICANT: Stone, David J.
		; APPLICANT: Verret, Corinne A. M.
		; APPLICANT: Voss, Edward Z.
		; APPLICANT: Zeitbauer, Bryan D.
		; TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method
		; FILE REFERENCE: 21402-377 B
		; CURRENT APPLICATION NUMBER: US/10/162-335
		; CURRENT FILING DATE: 2002-10-01
		; PRIOR APPLICATION NUMBER: 60/295,607
		; PRIOR FILING DATE: 2001-06-04
		; PRIOR APPLICATION NUMBER: 60/295,661
		; PRIOR FILING DATE: 2001-06-04

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// CURRENT APPLICATION NUMBER: US/10/162,335
// CURRENT FILING DATE: 2002-10-01
// PRIOR APPLICATION NUMBER: 60/295,607
// PRIOR FILING DATE: 2001-06-04
// PRIOR APPLICATION NUMBER: 60/295,661
// PRIOR FILING DATE: 2001-06-04
// PRIOR APPLICATION NUMBER: 60/295,404
// PRIOR FILING DATE: 2001-06-06
// PRIOR APPLICATION NUMBER: 60/295,418
// PRIOR FILING DATE: 2001-06-06
// PRIOR APPLICATION NUMBER: 60/297,414
// PRIOR FILING DATE: 2001-06-11
// PRIOR APPLICATION NUMBER: 60/297,567
// PRIOR FILING DATE: 2001-06-12
// PRIOR APPLICATION NUMBER: 60/298,285
// PRIOR FILING DATE: 2001-06-14
// PRIOR APPLICATION NUMBER: 60/298,556
// PRIOR FILING DATE: 2001-06-15
// PRIOR APPLICATION NUMBER: 60/299,949
// PRIOR FILING DATE: 2001-06-01
// PRIOR APPLICATION NUMBER: 60/300,883
// PRIOR FILING DATE: 2001-06-26
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 201
SEQ ID NO: 82
TYPE: PRT
ORGANISM: Homo sapiens
US-10-162-335-82

Query Match 100.0%; Score 660; DB 15; Length 390;
Best Local Similarity 100.0%; Pred. No. 2.9e-64;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Match 1  GKDFVQOPTKICVGCPRDIPNTSPELEETLTTITKLNAENNATYFKIDNVKARQVV 60
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
        216  GKDFVQOPTKICVGCPRDIPNTSPELEETLTTITKLNAENNATYFKIDNVKARQVV 275
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Match 2  61 AGKKYFIDFVARETTCSKESNEELTESCTKLQGOSLDCLNEAVVTPWEKKIYPTVNCQ 120
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
        276 AGKKYFIDFVARETTCSKESNEELTESCTKLQGOSLDCLNAEVVYPWEKKIYPTVNCQ 335
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Match 3  121 LGN 123
        ||| |
        336 LGM 338
        ||| |

RESULT 2
Sequence 70, Application US/10162335
Publication No. US20040094801A1
GENERAL INFORMATION:
APPLICANT: Anderson, David W.
APPLICANT: Baumgartner, Jason C.
APPLICANT: Boldog, Ferenc L.
APPLICANT: Casman, Stacie J.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Gangoli, Bsha A.
APPLICANT: Gerlach, Valerie
APPLICANT: Gorman, Linda
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Hjalt, Tord
APPLICANT: Kekuda, Ramesh
APPLICANT: Li, Li
APPLICANT: MacDoogall, John R.
APPLICANT: Malanykar, Uriel M.
APPLICANT: Miller, Isabelle
APPLICANT: Padigaru, Muralidhara
APPLICANT: Patturajan, Meera
APPLICANT: Pena, Carol E. A.
APPLICANT: Rastelli, Luca
APPLICANT: Shimer, Richard A.
APPLICANT: Stone, David J.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Verner, Corine A. M.
APPLICANT: Voss, Edward Z.
APPLICANT: Zerhusen, Bryan D.

TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method
FILE REFERENCE: 21402-377 B

// CURRENT APPLICATION NUMBER: US/10/162,335
// CURRENT FILING DATE: 2002-10-01
// PRIOR APPLICATION NUMBER: 60/295,607
// PRIOR FILING DATE: 2001-06-04
// PRIOR APPLICATION NUMBER: 60/295,661
// PRIOR FILING DATE: 2001-06-04
// PRIOR APPLICATION NUMBER: 60/297,404
// PRIOR FILING DATE: 2001-06-06
// PRIOR APPLICATION NUMBER: 60/295,418
// PRIOR FILING DATE: 2001-06-06
// PRIOR APPLICATION NUMBER: 60/297,414
// PRIOR FILING DATE: 2001-06-11
// PRIOR APPLICATION NUMBER: 60/297,567
// PRIOR FILING DATE: 2001-06-12
// PRIOR APPLICATION NUMBER: 60/298,285
// PRIOR FILING DATE: 2001-06-14
// PRIOR APPLICATION NUMBER: 60/298,556
// PRIOR FILING DATE: 2001-06-15
// PRIOR APPLICATION NUMBER: 60/299,949
// PRIOR FILING DATE: 2001-06-21
// PRIOR APPLICATION NUMBER: 60/300,883
// PRIOR FILING DATE: 2001-06-26
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 201
SEQ ID NO: 70
TYPE: PRT
ORGANISM: Homo sapiens
US-10-162-335-70

Query Match 100.0%; Score 660; DB 15; Length 398;
Best Local Similarity 100.0%; Pred. No. 3e-64;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Match 1  1 GKDFFVOPPTKICVGCRDIPNTSPELEETLTTITKLNAENNATYFKIDNVKARQVV 60
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
        224 GKDFFVOPPTKICVGCRDIPNTSPELEETLTTITKLNAENNATYFKIDNVKARQVV 283
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 61 AGKKYFIDFVARETTCSKESNEELTESCTKLQGOSLDCLNEAVVTPWEKKIYPTVNCQ 120
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
        284 AGKKYFIDFVARETTCSKESNEELTESCTKLQGOSLDCLNAEVVYPWEKKIYPTVNCQ 343
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 121 LGM 123
        ||| |
Db 344 LGM 346
        ||| |

RESULT 3
US-09-919-039-29
Sequence 29, Application US/09919039
Publication No. US20030108871A1
GENERAL INFORMATION:
APPLICANT: Kaser, Matthew R.
APPLICANT: Kaser, Matthew R.
FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
SEQ ID NO: 29
LENGTH: 427
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: misc_feature
OTHER INFORMATION: Incyte ID No. US20030108871A1 167507CD1
US-09-919-039-29

Query Match 100.0%; Score 660; DB 10; Length 427;
Best Local Similarity 100.0%; Pred. No. 3e-64;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 GKDVFQPTKTCVGCPRDIPTN SPELETITKLNAENNATYFKIDNVKKARQVV 60
 253 GKDVFQPTKTCVGCPRDIPTN SPELETITKLNAENNATYFKIDNVKKARQVV 312
 61 AGKKYFIDFVARETTCSKESNEELATESCTKLGSOLDCNAEVYYVWEEKIYPTVNCCP 120
 313 AGKKYFIDFVARETTCSKESNEELATESCTKLGSOLDCNAEVYYVWEEKIYPTVNCCP 372
 121 LGM 123
 373 LGM 375

RESULT 4
 US-10-162-335-72
 / Sequence 72, Application US/10162335
 / Publication No. US20040009450A1
 / GENERAL INFORMATION:
 / APPLICANT: Anderson, David W.
 / APPLICANT: Baumgartner, Jason C.
 / APPLICANT: Boldog, Ferenc L.
 / APPLICANT: Casman, Stacie J.
 / APPLICANT: Edinger, Shlomit R.
 / APPLICANT: Gangoli, Esha A.
 / APPLICANT: Gerlich, Valerie
 / APPLICANT: Gorman, Linda
 / APPLICANT: Guo, Xiaotia (Sasha)
 / APPLICANT: Hjalt, Tord
 / APPLICANT: Kekuda, Ramesh
 / APPLICANT: Li, Li
 / APPLICANT: MacDougall, John R.
 / APPLICANT: Malyankar, Uriel M.
 / APPLICANT: Miller, Isabelle
 / APPLICANT: Padigaru, Muralidhara
 / APPLICANT: Pattrajan, Meera
 / APPLICANT: Pena, Carol B. A.
 / APPLICANT: Rastelli, Luca
 / APPLICANT: Shimkets, Richard A.
 / APPLICANT: Stone, David J.
 / APPLICANT: Spytek, Kimberly A.
 / APPLICANT: Vernet, Corine A. M.
 / APPLICANT: Voss, Edward Z.
 / TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method
 / FILE REFERENCE: 21402-377 B
 / CURRENT APPLICATION NUMBER: US/10/162,335
 / CURRENT FILING DATE: 2002-10-01
 / PRIOR APPLICATION NUMBER: 60/295,607
 / PRIOR FILING DATE: 2001-06-14
 / PRIOR APPLICATION NUMBER: 60/295,661
 / PRIOR FILING DATE: 2001-06-04
 / PRIOR APPLICATION NUMBER: 60/295,404
 / PRIOR FILING DATE: 2001-06-06
 / PRIOR APPLICATION NUMBER: 60/296,418
 / PRIOR FILING DATE: 2001-06-14
 / PRIOR APPLICATION NUMBER: 60/298,556
 / PRIOR FILING DATE: 2001-06-15
 / PRIOR APPLICATION NUMBER: 60/297,567
 / PRIOR FILING DATE: 2001-06-12
 / PRIOR APPLICATION NUMBER: 60/298,285
 / PRIOR FILING DATE: 2001-06-14
 / PRIOR APPLICATION NUMBER: 60/297,414
 / PRIOR FILING DATE: 2001-06-11
 / PRIOR APPLICATION NUMBER: 60/297,567
 / PRIOR FILING DATE: 2001-06-11
 / PRIOR APPLICATION NUMBER: 60/300,883
 / PRIOR FILING DATE: 2001-06-26
 Remaining Prior Application data removed - See File Wrapper or PAML.

NUMBER OF SEQ ID NOS: 201
 SEQ ID NO: 72
 LENGTH: 615
 TYPE: PRT

; ORGANISM: Homo sapiens
 ; US-10-162-335-72
 Query Match 100.0%; Score 660; DB 15;
 Best Local Similarity 100.0%; Pred. No. 5.4e-64;
 Matches 123; Conservative 0; Mismatches 0;
 Indexes 0; Gaps 0;
 1 GKDVFQPTKTCVGCPRDIPTN SPELETITKLNAENNATYFKIDNVKKARQVV 60
 224 GKDVFQPTKTCVGCPRDIPTN SPELETITKLNAENNATYFKIDNVKKARQVV 283
 Qy 61 AGKKYFIDFVARETTCSKESNEELATESCTKLGSOLDCNAEVYYVWEEKIYPTVNCCP 120
 Db 284 AGKKYFIDFVARETTCSKESNEELATESCTKLGSOLDCNAEVYYVWEEKIYPTVNCCP 343
 Qy 121 LGM 123
 Db 344 LGM 346

RESULT 5
 US-10-162-335-74
 / Sequence 74, Application US/10162335
 / Publication No. US20040009480A1
 / GENERAL INFORMATION:
 / APPLICANT: Anderson, David W.
 / APPLICANT: Baumgartner, Jason C.
 / APPLICANT: Boldog, Ferenc L.
 / APPLICANT: Casman, Stacie J.
 / APPLICANT: Edinger, Shlomit R.
 / APPLICANT: Gangoli, Esha A.
 / APPLICANT: Gerlich, Valerie
 / APPLICANT: Gorman, Linda
 / APPLICANT: Guo, Xiaotia (Sasha)
 / APPLICANT: Hjalt, Tord
 / APPLICANT: Kekuda, Ramesh
 / APPLICANT: Li, Li
 / APPLICANT: MacDougall, John R.
 / APPLICANT: Malyankar, Uriel M.
 / APPLICANT: Miller, Isabelle
 / APPLICANT: Padigaru, Muralidhara
 / APPLICANT: Pattrajan, Meera
 / APPLICANT: Pena, Carol B. A.
 / APPLICANT: Rastelli, Luca
 / APPLICANT: Shimkets, Richard A.
 / APPLICANT: Stone, David J.
 / APPLICANT: Spytek, Kimberly A.
 / APPLICANT: Vernet, Corine A. M.
 / APPLICANT: Voss, Edward Z.
 / APPLICANT: Zethusen, Bryan D.
 / TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method
 / FILE REFERENCE: 21402-377 B
 / CURRENT APPLICATION NUMBER: US/10/162,335
 / CURRENT FILING DATE: 2002-10-01
 / PRIOR APPLICATION NUMBER: 60/295,607
 / PRIOR FILING DATE: 2001-06-04
 / PRIOR APPLICATION NUMBER: 60/295,661
 / PRIOR FILING DATE: 2001-06-04
 / PRIOR APPLICATION NUMBER: 60/295,404
 / PRIOR FILING DATE: 2001-06-06
 / PRIOR APPLICATION NUMBER: 60/296,418
 / PRIOR FILING DATE: 2001-06-14
 / PRIOR APPLICATION NUMBER: 60/298,556
 / PRIOR FILING DATE: 2001-06-15
 / PRIOR APPLICATION NUMBER: 60/297,567
 / PRIOR FILING DATE: 2001-06-11
 / PRIOR APPLICATION NUMBER: 60/297,567
 / PRIOR FILING DATE: 2001-06-12
 / PRIOR APPLICATION NUMBER: 60/298,285
 / PRIOR FILING DATE: 2001-06-14
 / PRIOR APPLICATION NUMBER: 60/297,414
 / PRIOR FILING DATE: 2001-06-11
 / PRIOR APPLICATION NUMBER: 60/297,567
 / PRIOR FILING DATE: 2001-06-12
 / PRIOR APPLICATION NUMBER: 60/298,285
 / PRIOR FILING DATE: 2001-06-14
 / PRIOR APPLICATION NUMBER: 60/298,556
 / PRIOR FILING DATE: 2001-06-15
 / PRIOR APPLICATION NUMBER: 60/299,949
 / PRIOR FILING DATE: 2001-06-11
 / PRIOR APPLICATION NUMBER: 60/300,883
 / PRIOR FILING DATE: 2001-06-26
 Remaining Prior Application data removed - See File Wrapper or PAML.

NUMBER OF SEQ ID NOS: 201
 SEQ ID NO: 72
 LENGTH: 615
 TYPE: PRT

PRIOR FILING DATE: 2001-06-26 ; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 201
; SEQ ID NO: 74
; LENGTH: 644
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-162-335-74

Query Match 100.0%; Score 660; DB 15; Length 644;
Best Local Similarity 100.0%; Pred. No. 5.7e-64;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKDFVQPPETKICVGCPRDIPNTSPELEBTLTTIKUNAENNATYFKIDNVKKARVQVV 60
Db 253 GKDFVQPPETKICVGCPRDIPNTSPELEBTLTTIKUNAENNATYFKIDNVKKARVQVV 312

Qy 61 AGKRYFIDFVARETTCSKESNELLTESETKLQGQSDUCNAEVVVYPWERKRYPTVNQCP 120
Db 313 AGKRYFIDFVARETTCSKESNELLTESETKLQGQSDUCNAEVVVYPWERKRYPTVNQCP 372

Qy 121 LGM 123

Db 373 LGM 375

RESULT 6
US-10-162-335-84
; Sequence 84, Application US/10162335
; GENERAL INFORMATION:
; Publication No. US20040094801
; APPLICANT: Anderson, David W.
; APPLICANT: Baumgartner, Jason C.
; APPLICANT: Bolodog, Ferenc L.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Hjalt, Tord
; APPLICANT: Rekuda, Ramesh
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Maralidhara
; APPLICANT: Patterson, Meera
; APPLICANT: Pena, Carol B. A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Voss, Edward Z.

TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method
FILE REFERENCE: 21402-377 B
CURRENT APPLICATION NUMBER: US/10/162,335
CURRENT FILING DATE: 2002-10-01

PRIOR APPLICATION NUMBER: 60/295,607
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/295,661
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/296,404
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/296,418
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/297,414
PRIOR FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 60/297,567
PRIOR FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: 60/298,285

PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/298,556
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/299,949
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/300,883
; PRIOR FILING DATE: 2001-06-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 201
; SEQ ID NO: 64
; LENGTH: 644
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-162-335-84

Query Match 100.0%; Score 660; DB 15; Length 644;
Best Local Similarity 100.0%; Pred. No. 5.7e-64;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKDFVQPPETKICVGCPRDIPNTSPELEBTLTTIKUNAENNATYFKIDNVKKARVQVV 60
Db 253 GKDFVQPPETKICVGCPRDIPNTSPELEBTLTTIKUNAENNATYFKIDNVKKARVQVV 312

Qy 61 AGKRYFIDFVARETTCSKESNELLTESETKLQGQSDUCNAEVVVYPWERKRYPTVNQCP 120
Db 313 AGKRYFIDFVARETTCSKESNELLTESETKLQGQSDUCNAEVVVYPWERKRYPTVNQCP 372

Qy 121 LGM 123

Db 373 LGM 375

RESULT 7
US-10-316-253-217
; Sequence 217, Application US/10316253
; Publication No. US20030162703A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8863M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 217
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; NUMBER OF SEQ ID NOS: 217

Query Match 60.9%; Score 402; DB 14; Length 424;
Best Local Similarity 61.8%; Pred. No. 1.1e-35;
Matches 14; Conservative 33; Mismatches 33; Indels 0; Gaps 0;

Qy 1 GKDFVQPPETKICVGCPRDIPNTSPELEBTLTTIKUNAENNATYFKIDNVKKARVQVV 60
Db 246 GDDLFELPFKNCGGCPREPVDSPPEALGHSIARNQAHNFIFKIDNVKKARVQVV 305

Qy 61 AGKRYFIDFVARETTCSKESNELLTESETKLQGQSDUCNAEVVVYPWERKRYPTVNQCP 120
Db 306 AGVIVYFLAREBINSQSKELETADCETRKLQGQSDUCNAEVVVYPWERKRYPTVNQCPA 365

Qy 121 LGM 123

Db 366 LDM 368

```

RESULT 8
US-10-316-215
; Sequence 215, Application US/10316253
; Publication No. US20050162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIORITY NUMBER: US 60/355,295
; PRIORITY FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 215
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-10-316-253-215

Query Match          Score 401; DB 14; Length 430;
Best Local Similarity 61.8%; Pred. No. 1.5e-35;
Matches 76; Conservative 14; Mismatches 33; Indels 0; Gaps 0;
Length 430;

Qy      1 GKDFFVQPPTKICVGCPDRDPTNSPELEETHTHTKLNAAENNATPFYFKIDNVKKARQVV 60
Db      252 GDDLFPLPKNCRGCREIPDPSPEKEAIGHSTIAQLNAOHNFHIFTYFKIDTVKCATSQVW 311
Qy      61 AGKRYFIDFYARETTGSKESNEELTSCTKKGOLDCAEAIVYPWEEKKIYPTVNCQP 120
Db      312 AGVIVYTFIARETNSKQSKTELADCCETKHLGQSLNLCAANVMPWENKVYPRVCQA 371

Qy      121 LGM 123
Db      372 LDM 374

RESULT 9
US-03-969-834-1
; Sequence 1, Application US/09969834
; Patent No. US20020102711A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surja K.
; TITLE OF INVENTION: NOVEL HUMAN CYSTATIN-LIKE PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq For Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/969,834
; FILING DATE: 01-Oct-2001
; CLASSIFICATION: <Unknown>

PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/471,765
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/791,522
FILING DATE: <Unknown>
APPLICATION NUMBER: 09/471,765

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Sequence 197, Application US/09746783
 Publication No. US20030044935A1
 GENERAL INFORMATION:
 APPLICANT: Jacobs, Kenneth
 McCoy, John M.
 LaVallie, Edward R.
 Racine, Lisa A.
 Tracy, Maurice
 Agostino, Michael J.
 Howes, Steven H.
 Pechele, Kim
 TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
 ENCODING THEM
 NUMBER OF SEQUENCES: 231
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genetics Institute, Inc.
 STREET: 87 Cambridge Park Drive
 CITY: Cambridge
 STATE: MA
 COUNTRY: U.S.A.
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/746,783
 FILING DATE: 21-Dec-2000
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Milasincic, Debra J.
 REGISTRATION NUMBER: 46,931
 TELEPHONE: (617) 227-4240
 TELEFAX: (617) 742-4214
 INFORMATION FOR SEQ ID NO: 197:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 167 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 197:
 US 09-746-783-197

Query Match 25.1%; Score 165.5; DB 10; Length 167;
 Best Local Similarity 32.5%; Pred. No. 4,7e-10;
 Matches 37; Conservative 22; Mismatches 50; Indels 5; Gaps 3;

Qy 9 TKTCVGGPDIPTNSPELETLTITKLNAENNAFPYKFLDNVKARQVAGKPYID 68
 Db 54 SRVKGPFKTIKNDPGVHQARYSTKEFNNTNDMFLERESRITALVQVKGLKYMLE 113

Qy 69 FVARETTCSKESNBELTSCB ---TKRLGQSLDNCNAEVVYPPWEEKI -YPTPTNC 118
 Db 114 VEIGRTICKNQHRL-DDCDFTQTNHTLQKQTLSCYSEWWVTPWLQHFEVPPVLR 166

RESULT 12
 US-09-775-932-14
 Sequence 14, Application US/0975932
 Patent No. US2002013671A1
 GENERAL INFORMATION:
 APPLICANT: University of British Columbia
 TITLE OF INVENTION: Production and use of Modified Cystatins
 FILE REFERENCE: 58069
 CURRENT APPLICATION NUMBER: US/09/775-932
 CURRENT FILING DATE: 2001-02-02
 PRIOR APPLICATION NUMBER: CA99/00717
 PRIOR FILING DATE: 1999-08-05
 PRIOR APPLICATION NUMBER: 58069
 PRIOR FILING DATE: 1998-08-15
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 12
 LENGTH: 128
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-775-932-12

Query Match 21.0%; Score 138.5; DB 9; Length 121;
 Best Local Similarity 31.5%; Pred. No. 3e-07;
 Matches 34; Conservative 22; Mismatches 45; Indels 7; Gaps 3;

Qy 8 PTKICVGCPDIPTNSPELETLTITKLNAENNAFPYKFLDNVKARQVAGKPYID 67
 Db 2 PQERMVGEIRDLSPPDPQVKQAQAAVASYNGSNSYYFRDTHIKAQSQLVAGKPYID 61

Qy 68 FVARETTCSKE ---SNEELTESCETKQLGQ -SLDCNAEVVYPPME 109
 Db 62 TMENGSTDCKTRVGTGDHVDLT -TCPPLAAGAQEQEKLRCDFEVLVVPHQ 108

RESULT 13
 US-09-775-932-12
 Sequence 12, Application US/0975932
 Patent No. US20020137671A1
 GENERAL INFORMATION:
 APPLICANT: University of British Columbia
 TITLE OF INVENTION: Production and use of Modified Cystatins
 FILE REFERENCE: 58069
 CURRENT APPLICATION NUMBER: US/09/775-932
 CURRENT FILING DATE: 2001-02-02
 PRIOR APPLICATION NUMBER: CA99/00717
 PRIOR FILING DATE: 1999-08-05
 PRIOR APPLICATION NUMBER: 58069
 PRIOR FILING DATE: 1998-08-15
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 12
 LENGTH: 128
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-775-932-12

Query Match 21.0%; Score 138.5; DB 9; Length 128;
 Best Local Similarity 31.5%; Pred. No. 3,2e-07;
 Matches 34; Conservative 22; Mismatches 45; Indels 7; Gaps 3;

Qy 8 PTKICVGCPDIPTNSPELETLTITKLNAENNAFPYKFLDNVKARQVAGKPYID 67
 Db 9 PQERMVGEIRDLSPPDPQVKQAQAAVASYNGSNSYYFRDTHIKAQSQLVAGKPYID 68

Qy 68 FVARETTCSKE ---SNEELTESCETKQLGQ -SLDCNAEVVYPPME 109
 Db 69 TMENGSTDCKTRVGTGDHVDLT -TCPPLAAGAQEQEKLRCDFEVLVVPHQ 115

RESULT 14
 US-09-940-497-2
 Sequence 2, Application US/09940497
 Patent No. US20020132476A1
 GENERAL INFORMATION:
 APPLICANT: Ni et al.
 TITLE OF INVENTION: Human Cystatin E
 FILE REFERENCE: PE202P1D2
 CURRENT APPLICATION NUMBER: US/09/940,497
 CURRENT FILING DATE: 2001-08-29
 PRIOR APPLICATION NUMBER: US 09/241,376
 PRIOR FILING DATE: 1999-02-02
 PRIOR APPLICATION NUMBER: US 08/744,138
 PRIOR FILING DATE: 1996-11-05
 PRIOR APPLICATION NUMBER: US 08/461,030
 PRIOR FILING DATE: 1995-06-05

NUMBER OF SEQ ID NOS: 13
 SEQ ID NO 2
 LENGTH: 149
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-08-940-197-2

Query Match 21.0%; Score 138.5; DB 9; Length 149;
 Best Local Similarity 31.5%; Pred. No. 3.9e-07; Gaps 3;
 Matches 34; Conservative 22; Mismatches 45; Indels 7; Gaps 3;

Qy 8 PTKICVGCPRDIPNTSPEELTLTHITKLNAENNATFYKIDNYKKARYQVWAGKKYPI 67
 Db 30 POERMVGLDLSPPDFQVQAQAAVASTANGNSIYFRDTHIKAQSQLVAGCKYPL 89

Qy 68 DFWARETTCSKE---SNWELTEESCTKRGQ-SLDCHNEVIVVWPE 109
 Db 90 TMEMGSTDCCRTRVTGDPHVDLT-TCPLAGAQQEKLRCDFEVLYVWQ 136

RESULT 15
 US-08-849-303-16
 Sequence 16, Application US/0849303
 Publication No. US20030221209A1
 GENERAL INFORMATION:
 APPLICANT: Atkinson, Howard J.
 ATTORNEY: McPherson, Michael J.
 INVENTOR: Urwin, Peter E.
 TITLE OF INVENTION: MODIFIED PROTEINASE INHIBITORS
 NUMBER OF SEQUENCES: 79
 TITLE OF INVENTION: MODIFIED PROTEINASE INHIBITORS
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kluber & Jackson
 STREET: 411 Hackensack Avenue, 4th Floor
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/849,303
 FILING DATE: 21-MAY-1997
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 1321-1-003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-343-1684
 TELEX: 133521
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 112 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 US-08-849-303-16

Query Match 20.6%; Score 136; DB 8; Length 112;
 Best Local Similarity 30.6%; Pred. No. 5.1e-07; Gaps 5;
 Matches 34; Conservative 22; Mismatches 31; Indels 24; Gaps 5;

Qy 22 NSPELEETLTITKLNAENNATFYKIDNYKKARYQVWAGKKYRDFVARETTCSKEIN 81
 Db 12 NEEGVQEALSFASVSEFNKRSNDAYQSRVVRVRAKXQVSGMNFIDVBLGRITCTK-S 69

